

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: ALBERTSEN, HANS
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(ii) TITLE OF INVENTION: APC ANTIBODIES

(iii) NUMBER OF SEQUENCES: 102

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20001-4598

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/452,654
(B) FILING DATE: 25-MAY-1995

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/289,548
(B) FILING DATE: 12-AUG-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/741,940
(B) FILING DATE: 08-AUG-1991

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: 1107.78817

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9606 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: DP2.5 (APC)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 34..8562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGACTCGGAA ATGAGGTCCA AGGGTAGCCA AGG ATG GCT GCA GCT TCA TAT GAT 54
Met Ala Ala Ala Ser Tyr Asp
1 5
CAG TTG TTA AAG CAA GTT GAG GCA CTG AAG ATG GAG AAC TCA AAT CTT 102
Gln Leu Leu Lys Gln Val Glu Ala Leu Lys Met Glu Asn Ser Asn Leu
10 15 20
CGA CAA GAG CTA GAA GAT AAT TCC AAT CAT CTT ACA AAA CTG GAA ACT 150
Arg Gln Glu Leu Glu Asp Asn Ser Asn His Leu Thr Lys Leu Glu Thr
25 30 35
GAG GCA TCT AAT ATG AAG GAA GTA CTT AAA CAA CTA CAA GGA AGT ATT 198
Glu Ala Ser Asn Met Lys Glu Val Leu Lys Gln Leu Gln Gly Ser Ile
40 45 50 55
GAA GAT GAA GCT ATG GCT TCT TCT GGA CAG ATT GAT TTA TTA GAG CGT 246
Glu Asp Glu Ala Met Ala Ser Ser Gly Gln Ile Asp Leu Leu Glu Arg
60 65 70
CTT AAA GAG CTT AAC TTA GAT AGC AGT AAT TTC CCT GGA GTA AAA CTG 294
Leu Lys Glu Leu Asn Leu Asp Ser Ser Asn Phe Pro Gly Val Lys Leu
75 80 85
CGG TCA AAA ATG TCC CTC CGT TCT TAT GGA AGC CGG GAA GGA TCT GTA 342
Arg Ser Lys Met Ser Leu Arg Ser Tyr Gly Ser Arg Glu Gly Ser Val

AA14

09442439-1189

90	95	100	
TCA AGC CGT TCT GGA GAG TGC AGT CCT GTT CCT ATG GGT TCA TTT CCA			390
Ser Ser Arg Ser Gly Glu Cys Ser Pro Val Pro Met Gly Ser Phe Pro			
105	110	115	
AGA AGA GGG TTT GTA AAT GGA AGC AGA GAA AGT ACT GGA TAT TTA GAA			438
Arg Arg Gly Phe Val Asn Gly Ser Arg Glu Ser Thr Gly Tyr Leu Glu			
120	125	130	135
GAA CTT GAG AAA GAG AGG TCA TTG CTT CTT GCT GAT CTT GAC AAA GAA			486
Glu Leu Glu Lys Glu Arg Ser Leu Leu Ala Asp Leu Asp Lys Glu			
140	145	150	
GAA AAG GAA AAA GAC TGG TAT TAC GCT CAA CTT CAG AAT CTC ACT AAA			534
Glu Lys Glu Lys Asp Trp Tyr Tyr Ala Gln Leu Gln Asn Leu Thr Lys			
155	160	165	
AGA ATA GAT AGT CTT CCT TTA ACT GAA AAT TTT TCC TTA CAA ACA GAT			582
Arg Ile Asp Ser Leu Pro Leu Thr Glu Asn Phe Ser Leu Gln Thr Asp			
170	175	180	
TTG ACC AGA AGG CAA TTG GAA TAT GAA GCA AGG CAA ATC AGA GTT GCG			630
Leu Thr Arg Arg Gln Leu Glu Tyr Glu Ala Arg Gln Ile Arg Val Ala			
185	190	195	
ATG GAA GAA CAA CTA GGT ACC TGC CAG GAT ATG GAA AAA CGA GCA CAG			678
Met Glu Glu Gln Leu Gly Thr Cys Gln Asp Met Glu Lys Arg Ala Gln			
200	205	210	215
CGA AGA ATA GCC AGA ATT CAG CAA ATC GAA AAG GAC ATA CTT CGT ATA			726
Arg Arg Ile Ala Arg Ile Gln Gln Ile Glu Lys Asp Ile Leu Arg Ile			
220	225	230	
CGA CAG CTT TTA CAG TCC CAA GCA ACA GAA GCA GAG AGG TCA TCT CAG			774
Arg Gln Leu Leu Gln Ser Gln Ala Thr Glu Ala Glu Arg Ser Ser Gln			
235	240	245	
AAC AAG CAT GAA ACC GGC TCA CAT GAT GCT GAG CGG CAG AAT GAA GGT			822
Asn Lys His Glu Thr Gly Ser His Asp Ala Glu Arg Gln Asn Glu Gly			
250	255	260	
CAA GGA GTG GGA GAA ATC AAC ATG GCA ACT TCT GGT AAT GGT CAG GGT			870
Gln Gly Val Gly Glu Ile Asn Met Ala Thr Ser Gly Asn Gly Gln Gly			
265	270	275	
TCA ACT ACA CGA ATG GAC CAT GAA ACA GCC AGT GTT TTG AGT TCT AGT			918
Ser Thr Thr Arg Met Asp His Glu Thr Ala Ser Val Leu Ser Ser Ser			
280	285	290	295
AGC ACA CAC TCT GCA CCT CGA AGG CTG ACA AGT CAT CTG GGA ACC AAG			966
Ser Thr His Ser Ala Pro Arg Arg Leu Thr Ser His Leu Gly Thr Lys			
300	305	310	
GTG GAA ATG GTG TAT TCA TTG TTG TCA ATG CTT GGT ACT CAT GAT AAG			1014

Val Glu Met Val Tyr Ser Leu Leu Ser Met Leu Gly Thr His Asp Lys
 315 320 325

GAT GAT ATG TCG CGA ACT TTG CTA GCT ATG TCT AGC TCC CAA GAC AGC 1062
 Asp Asp Met Ser Arg Thr Leu Leu Ala Met Ser Ser Ser Gln Asp Ser
 330 335 340

TGT ATA TCC ATG CGA CAG TCT GGA TGT CTT CCT CTC CTC ATC CAG CTT 1110
 Cys Ile Ser Met Arg Gln Ser Gly Cys Leu Pro Leu Leu Ile Gln Leu
 345 350 355

TTA CAT GGC AAT GAC AAA GAC TCT GTA TTG TTG GGA AAT TCC CGG GGC 1158
 Leu His Gly Asn Asp Lys Asp Ser Val Leu Leu Gly Asn Ser Arg Gly
 360 365 370 375

AGT AAA GAG GCT CGG GCC AGG GCC AGT GCA GCA CTC CAC AAC ATC ATT 1206
 Ser Lys Glu Ala Arg Ala Arg Ala Ser Ala Ala Leu His Asn Ile Ile
 380 385 390

CAC TCA CAG CCT GAT GAC AAG AGA GGC AGG CGT GAA ATC CGA GTC CTT 1254
 His Ser Gln Pro Asp Asp Lys Arg Gly Arg Arg Glu Ile Arg Val Leu
 395 400 405

CAT CTT TTG GAA CAG ATA CGC GCT TAC TGT GAA ACC TGT TGG GAG TGG 1302
 His Leu Leu Glu Gln Ile Arg Ala Tyr Cys Glu Thr Cys Trp Glu Trp
 410 415 420

CAG GAA GCT CAT GAA CCA GGC ATG GAC CAG GAC AAA AAT CCA ATG CCA 1350
 Gln Glu Ala His Glu Pro Gly Met Asp Gln Asp Lys Asn Pro Met Pro
 425 430 435

GCT CCT GTT GAA CAT CAG ATC TGT CCT GCT GTG TGT GTT CTA ATG AAA 1398
 Ala Pro Val Glu His Gln Ile Cys Pro Ala Val Cys Val Leu Met Lys
 440 445 450 455

CTT TCA TTT GAT GAA GAG CAT AGA CAT GCA ATG AAT GAA CTA GGG GGA 1446
 Leu Ser Phe Asp Glu Glu His Arg His Ala Met Asn Glu Leu Gly Gly
 460 465 470

CTA CAG GCC ATT GCA GAA TTA TTG CAA GTG GAC TGT GAA ATG TAT GGG 1494
 Leu Gln Ala Ile Ala Glu Leu Leu Gln Val Asp Cys Glu Met Tyr Gly
 475 480 485

CTT ACT AAT GAC CAC TAC AGT ATT ACA CTA AGA CGA TAT GCT GGA ATG 1542
 Leu Thr Asn Asp His Tyr Ser Ile Thr Leu Arg Arg Tyr Ala Gly Met
 490 495 500

GCT TTG ACA AAC TTG ACT TTT GGA GAT GTA GCC AAC AAG GCT ACG CTA 1590
 Ala Leu Thr Asn Leu Thr Phe Gly Asp Val Ala Asn Lys Ala Thr Leu
 505 510 515

TGC TCT ATG AAA GGC TGC ATG AGA GCA CTT GTG GCC CAA CTA AAA TCT 1638
 Cys Ser Met Lys Gly Cys Met Arg Ala Leu Val Ala Gln Leu Lys Ser
 520 525 530 535

GAA AGT GAA GAC TTA CAG CAG GTT ATT GCA AGT GTT TTG AGG AAT TTG 1686
 Glu Ser Glu Asp Leu Gln Gln Val Ile Ala Ser Val Leu Arg Asn Leu
 540 545 550
 TCT TGG CGA GCA GAT GTA AAT AGT AAA AAG ACG TTG CGA GAA GTT GGA 1734
 Ser Trp Arg Ala Asp Val Asn Ser Lys Lys Thr Leu Arg Glu Val Gly
 555 560 565
 AGT GTG AAA GCA TTG ATG GAA TGT GCT TTA GAA GTT AAA AAG GAA TCA 1782
 Ser Val Lys Ala Leu Met Glu Cys Ala Leu Glu Val Lys Lys Glu Ser
 570 575 580
 ACC CTC AAA AGC GTA TTG AGT GCC TTA TGG AAT TTG TCA GCA CAT TGC 1830
 Thr Leu Lys Ser Val Leu Ser Ala Leu Trp Asn Leu Ser Ala His Cys
 585 590 595
 ACT GAG AAT AAA GCT GAT ATA TGT GCT GTA GAT GGT GCA CTT GCA TTT 1878
 Thr Glu Asn Lys Ala Asp Ile Cys Ala Val Asp Gly Ala Leu Ala Phe
 600 605 610 615
 TTG GTT GGC ACT CTT ACT TAC CGG AGC CAG ACA AAC ACT TTA GCC ATT 1926
 Leu Val Gly Thr Leu Thr Tyr Arg Ser Gln Thr Asn Thr Leu Ala Ile
 620 625 630
 ATT GAA AGT GGA GGT GGG ATA TTA CGG AAT GTG TCC AGC TTG ATA GCT 1974
 Ile Glu Ser Gly Gly Gly Ile Leu Arg Asn Val Ser Ser Leu Ile Ala
 635 640 645
 ACA AAT GAG GAC CAC AGG CAA ATC CTA AGA GAG AAC AAC TGT CTA CAA 2022
 Thr Asn Glu Asp His Arg Gln Ile Leu Arg Glu Asn Asn Cys Leu Gln
 650 655 660
 ACT TTA TTA CAA CAC TTA AAA TCT CAT AGT TTG ACA ATA GTC AGT AAT 2070
 Thr Leu Leu Gln His Leu Lys Ser His Ser Leu Thr Ile Val Ser Asn
 665 670 675
 GCA TGT GGA ACT TTG TGG AAT CTC TCA GCA AGA AAT CCT AAA GAC CAG 2118
 Ala Cys Gly Thr Leu Trp Asn Leu Ser Ala Arg Asn Pro Lys Asp Gln
 680 685 690 695
 GAA GCA TTA TGG GAC ATG GGG GCA GTT AGC ATG CTC AAG AAC CTC ATT 2166
 Glu Ala Leu Trp Asp Met Gly Ala Val Ser Met Leu Lys Asn Leu Ile
 700 705 710
 CAT TCA AAG CAC AAA ATG ATT GCT ATG GGA AGT GCT GCA GCT TTA AGG 2214
 His Ser Lys His Lys Met Ile Ala Met Gly Ser Ala Ala Ala Leu Arg
 715 720 725
 AAT CTC ATG GCA AAT AGG CCT GCG AAG TAC AAG GAT GCC AAT ATT ATG 2262
 Asn Leu Met Ala Asn Arg Pro Ala Lys Tyr Lys Asp Ala Asn Ile Met
 730 735 740
 TCT CCT GGC TCA AGC TTG CCA TCT CTT CAT GTT AGG AAA CAA AAA GCC 2310
 Ser Pro Gly Ser Ser Leu Pro Ser Leu His Val Arg Lys Gln Lys Ala
 745 750 755

CTA GAA GCA GAA TTA GAT GCT CAG CAC TTA TCA GAA ACT TTT GAC AAT 2358
 Leu Glu Ala Glu Leu Asp Ala Gln His Leu Ser Glu Thr Phe Asp Asn 775
 760 765 770
 ATA GAC AAT TTA AGT CCC AAG GCA TCT CAT CGT AGT AAG CAG AGA CAC 2406
 Ile Asp Asn Leu Ser Pro Lys Ala Ser His Arg Ser Lys Gln Arg His 790
 780 785
 AAG CAA AGT CTC TAT GGT GAT TAT GTT TTT GAC ACC AAT CGA CAT GAT 2454
 Lys Gln Ser Leu Tyr Gly Asp Tyr Val Phe Asp Thr Asn Arg His Asp 805
 795 800
 GAT AAT AGG TCA GAC AAT TTT AAT ACT GGC AAC ATG ACT GTC CTT TCA 2502
 Asp Asn Arg Ser Asp Asn Phe Asn Thr Gly Asn Met Thr Val Leu Ser 820
 810 815
 CCA TAT TTG AAT ACT ACA GTG TTA CCC AGC TCC TCT TCA TCA AGA GGA 2550
 Pro Tyr Leu Asn Thr Thr Val Leu Pro Ser Ser Ser Ser Ser Arg Gly 835
 825 830
 AGC TTA GAT AGT TCT CGT TCT GAA AAA GAT AGA AGT TTG GAG AGA GAA 2598
 Ser Leu Asp Ser Ser Arg Ser Glu Lys Asp Arg Ser Leu Glu Arg Glu 855
 840 845 850
 CGC GGA ATT GGT CTA GGC AAC TAC CAT CCA GCA ACA GAA AAT CCA GGA 2646
 Arg Gly Ile Gly Leu Gly Asn Tyr His Pro Ala Thr Glu Asn Pro Gly 870
 860 865
 ACT TCT TCA AAG CGA GGT TTG CAG ATC TCC ACC ACT GCA GCC CAG ATT 2694
 Thr Ser Ser Lys Arg Gly Leu Gln Ile Ser Thr Thr Ala Ala Gln Ile 885
 875 880
 GCC AAA GTC ATG GAA GAA GTG TCA GGC ATT CAT ACC TCT CAG GAA GAC 2742
 Ala Lys Val Met Glu Glu Val Ser Ala Ile His Thr Ser Gln Glu Asp 900
 890 895
 AGA AGT TCT GGG TCT ACC ACT GAA TTA CAT TCT GTG ACA GAT GAG AGA 2790
 Arg Ser Ser Gly Ser Thr Thr Glu Leu His Cys Val Thr Asp Glu Arg 915
 905 910
 AAT GCA CTT AGA AGA AGC TCT GCT GCC CAT ACA CAT TCA AAC ACT TAC 2838
 Asn Ala Leu Arg Arg Ser Ser Ala Ala His Thr His Ser Asn Thr Tyr 935
 920 925 930
 AAT TTC ACT AAG TCG GAA AAT TCA AAT AGG ACA TGT TCT ATG CCT TAT 2886
 Asn Phe Thr Lys Ser Glu Asn Ser Asn Arg Thr Cys Ser Met Pro Tyr 950
 940 945
 GCC AAA TTA GAA TAC AAG AGA TCT TCA AAT GAT AGT TTA AAT AGT GTC 2934
 Ala Lys Leu Glu Tyr Lys Arg Ser Ser Asn Asp Ser Leu Asn Ser Val 965
 955 960
 AGT AGT AAT GAT GGT TAT GGT AAA AGA GGT CAA ATG AAA CCC TCG ATT 2982
 Ser Ser Asn Asp Gly Tyr Gly Lys Arg Gly Gln Met Lys Pro Ser Ile 980
 970 975

GAA TCC TAT TCT GAA GAT GAT GAA AGT AAG TTT TGC AGT TAT GGT CAA 3030
 Glu Ser Tyr Ser Glu Asp Asp Glu Ser Lys Phe Cys Ser Tyr Gly Gln
 985 990 995
 TAC CCA GCC GAC CTA GCC CAT AAA ATA CAT AGT GCA AAT CAT ATG GAT 3078
 Tyr Pro Ala Asp Leu Ala His Lys Ile His Ser Ala Asn His Met Asp
 1000 1005 1010 1015
 GAT AAT GAT GGA GAA CTA GAT ACA CCA ATA AAT TAT AGT CTT AAA TAT 3126
 Asp Asn Asp Gly Glu Leu Asp Thr Pro Ile Asn Tyr Ser Leu Lys Tyr
 1020 1025 1030
 TCA GAT GAG CAG TTG AAC TCT GGA AGG CAA AGT CCT TCA CAG AAT GAA 3174
 Ser Asp Glu Gln Leu Asn Ser Gly Arg Gln Ser Pro Ser Gln Asn Glu
 1035 1040 1045
 AGA TGG GCA AGA CCC AAA CAC ATA ATA GAA GAT GAA ATA AAA CAA AGT 3222
 Arg Trp Ala Arg Pro Lys His Ile Ile Glu Asp Glu Ile Lys Gln Ser
 1050 1055 1060
 GAG CAA AGA CAA TCA AGG AAT CAA AGT ACA ACT TAT CCT GTT TAT ACT 3270
 Glu Gln Arg Gln Ser Arg Asn Gln Ser Thr Thr Tyr Pro Val Tyr Thr
 1065 1070 1075
 GAG AGC ACT GAT GAT AAA CAC CTC AAG TTC CAA CCA CAT TTT GGA CAG 3318
 Glu Ser Thr Asp Asp Lys His Leu Lys Phe Gln Pro His Phe Gly Gln
 1080 1085 1090 1095
 CAG GAA TGT GTT TCT CCA TAC AGG TCA CGG GGA GCC AAT GGT TCA GAA 3366
 Gln Glu Cys Val Ser Pro Tyr Arg Ser Arg Gly Ala Asn Gly Ser Glu
 1100 1105 1110
 ACA AAT CGA GTG GGT TCT AAT CAT GGA ATT AAT CAA AAT GTA AGC CAG 3414
 Thr Asn Arg Val Gly Ser Asn His Gly Ile Asn Gln Asn Val Ser Gln
 1115 1120 1125
 TCT TTG TGT CAA GAA GAT GAC TAT GAA GAT GAT AAG CCT ACC AAT TAT 3462
 Ser Leu Cys Gln Glu Asp Asp Tyr Glu Asp Asp Lys Pro Thr Asn Tyr
 1130 1135 1140
 AGT GAA CGT TAC TCT GAA GAA GAA CAG CAT GAA GAA GAA GAG AGA CCA 3510
 Ser Glu Arg Tyr Ser Glu Glu Glu Gln His Glu Glu Glu Glu Arg Pro
 1145 1150 1155
 ACA AAT TAT AGC ATA AAA TAT AAT GAA GAG AAA CGT CAT GTG GAT CAG 3558
 Thr Asn Tyr Ser Ile Lys Tyr Asn Glu Glu Lys Arg His Val Asp Gln
 1160 1165 1170 1175
 CCT ATT GAT TAT AGT TTA AAA TAT GCC ACA GAT ATT CCT TCA TCA CAG 3606
 Pro Ile Asp Tyr Ser Leu Lys Tyr Ala Thr Asp Ile Pro Ser Ser Gln
 1180 1185 1190
 AAA CAG TCA TTT TCA TTC TCA AAG AGT TCA TCT GGA CAA AGC AGT AAA 3654
 Lys Gln Ser Phe Ser Phe Ser Lys Ser Ser Ser Gly Gln Ser Ser Lys
 1195 1200 1205

ACC GAA CAT ATG TCT TCA AGC AGT GAG AAT ACG TCC ACA CCT TCA TCT 3702
 Thr Glu His Met Ser Ser Ser Ser Glu Asn Thr Ser Thr Pro Ser Ser
 1210 1215 1220

AAT GCC AAG AGG CAG AAT CAG CTC CAT CCA AGT TCT GCA CAG AGT AGA 3750
 Asn Ala Lys Arg Gln Asn Gln Leu His Pro Ser Ser Ala Gln Ser Arg
 1225 1230 1235

AGT GGT CAG CCT CAA AAG GCT GCC ACT TGC AAA GTT TCT TCT ATT AAC 3798
 Ser Gly Gln Pro Gln Lys Ala Ala Thr Cys Lys Val Ser Ser Ile Asn
 1240 1245 1250 1255

CAA GAA ACA ATA CAG ACT TAT TGT GTA GAA GAT ACT CCA ATA TGT TTT 3846
 Gln Glu Thr Ile Gln Thr Tyr Cys Val Glu Asp Thr Pro Ile Cys Phe
 1260 1265 1270

TCA AGA TGT AGT TCA TTA TCA TCT TTG TCA TCA GCT GAA GAT GAA ATA 3894
 Ser Arg Cys Ser Ser Leu Ser Ser Leu Ser Ser Ala Glu Asp Glu Ile
 1275 1280 1285

GGA TGT AAT CAG ACG ACA CAG GAA GCA GAT TCT GCT AAT ACC CTG CAA 3942
 Gly Cys Asn Gln Thr Thr Gln Glu Ala Asp Ser Ala Asn Thr Leu Gln
 1290 1295 1300

ATA GCA GAA ATA AAA GGA AAG ATT GGA ACT AGG TCA GCT GAA GAT CCT 3990
 Ile Ala Glu Ile Lys Gly Lys Ile Gly Thr Arg Ser Ala Glu Asp Pro
 1305 1310 1315

GTG AGC GAA GTT CCA GCA GTG TCA CAG CAC CCT AGA ACC AAA TCC AGC 4038
 Val Ser Glu Val Pro Ala Val Ser Gln His Pro Arg Thr Lys Ser Ser
 1320 1325 1330 1335

AGA CTG CAG GGT TCT AGT TTA TCT TCA GAA TCA GCC AGG CAC AAA GCT 4086
 Arg Leu Gln Gly Ser Ser Leu Ser Ser Glu Ser Ala Arg His Lys Ala
 1340 1345 1350

GTT GAA TTT CCT TCA GGA GCG AAA TCT CCC TCC AAA AGT GGT GCT CAG 4134
 Val Glu Phe Pro Ser Gly Ala Lys Ser Pro Ser Lys Ser Gly Ala Gln
 1355 1360 1365

ACA CCC AAA AGT CCA CCT GAA CAC TAT GTT CAG GAG ACC CCA CTC ATG 4182
 Thr Pro Lys Ser Pro Pro Glu His Tyr Val Gln Glu Thr Pro Leu Met
 1370 1375 1380

TTT AGC AGA TGT ACT TCT GTC AGT TCA CTT GAT AGT TTT GAG AGT CGT 4230
 Phe Ser Arg Cys Thr Ser Val Ser Ser Leu Asp Ser Phe Glu Ser Arg
 1385 1390 1395

TCG ATT GCC AGC TCC GTT CAG AGT GAA CCA TGC AGT GGA ATG GTA AGT 4278
 Ser Ile Ala Ser Ser Val Gln Ser Glu Pro Cys Ser Gly Met Val Ser
 1400 1405 1410 1415

GGC ATT ATA AGC CCC AGT GAT CTT CCA GAT AGC CCT GGA CAA ACC ATG 4326
 Gly Ile Ile Ser Pro Ser Asp Leu Pro Asp Ser Pro Gly Gln Thr Met
 1420 1425 1430

CCA CCA AGC AGA AGT AAA ACA CCT CCA CCA CCT CCT CAA ACA GCT CAA 4374
Pro Pro Ser Arg Ser Lys Thr Pro Pro Pro Pro Pro Gln Thr Ala Gln
1435 1440 1445

ACC AAG CGA GAA GTA CCT AAA AAT AAA GCA CCT ACT GCT GAA AAG AGA 4422
Thr Lys Arg Glu Val Pro Lys Asn Lys Ala Pro Thr Ala Glu Lys Arg
1450 1455 1460

GAG AGT GGA CCT AAG CAA GCT GCA GTA AAT GCT GCA GTT CAG AGG GTC 4470
Glu Ser Gly Pro Lys Gln Ala Ala Val Asn Ala Ala Val Gln Arg Val
1465 1470 1475

CAG GTT CTT CCA GAT GCT GAT ACT TTA TTA CAT TTT GCC ACA GAA AGT 4518
Gln Val Leu Pro Asp Ala Asp Thr Leu Leu His Phe Ala Thr Glu Ser
1480 1485 1490 1495

ACT CCA GAT GGA TTT TCT TGT TCA TCC AGC CTG AGT GCT CTG AGC CTC 4566
Thr Pro Asp Gly Phe Ser Cys Ser Ser Ser Leu Ser Ala Leu Ser Leu
1500 1505 1510

GAT GAG CCA TTT ATA CAG AAA GAT GTG GAA TTA AGA ATA ATG CCT CCA 4614
Asp Glu Pro Phe Ile Gln Lys Asp Val Glu Leu Arg Ile Met Pro Pro
1515 1520 1525

GTT CAG GAA AAT GAC AAT GGG AAT GAA ACA GAA TCA GAG CAG CCT AAA 4662
Val Gln Glu Asn Asp Asn Gly Asn Glu Thr Glu Ser Glu Gln Pro Lys
1530 1535 1540

GAA TCA AAT GAA AAC CAA GAG AAA GAG GCA GAA AAA ACT ATT GAT TCT 4710
Glu Ser Asn Glu Asn Gln Glu Lys Glu Ala Glu Lys Thr Ile Asp Ser
1545 1550 1555

GAA AAG GAC CTA TTA GAT GAT TCA GAT GAT GAT GAT ATT GAA ATA CTA 4758
Glu Lys Asp Leu Leu Asp Asp Ser Asp Asp Asp Asp Ile Glu Ile Leu
1560 1565 1570 1575

GAA GAA TGT ATT ATT TCT GCC ATG CCA ACA AAG TCA TCA CGT AAA GGC 4806
Glu Glu Cys Ile Ile Ser Ala Met Pro Thr Lys Ser Ser Arg Lys Gly
1580 1585 1590

AAA AAG CCA GCC CAG ACT GCT TCA AAA TTA CCT CCA CCT GTG GCA AGG 4854
Lys Lys Pro Ala Gln Thr Ala Ser Lys Leu Pro Pro Pro Val Ala Arg
1595 1600 1605

AAA CCA AGT CAG CTG CCT GTG TAC AAA CTT CTA CCA TCA CAA AAC AGG 4902
Lys Pro Ser Gln Leu Pro Val Tyr Lys Leu Leu Pro Ser Gln Asn Arg
1610 1615 1620

TTG CAA CCC CAA AAG CAT GTT AGT TTT ACA CCG GGG GAT GAT ATG CCA 4950
Leu Gln Pro Gln Lys His Val Ser Phe Thr Pro Gly Asp Asp Met Pro
1625 1630 1635

CGG GTG TAT TGT GTT GAA GGG ACA CCT ATA AAC TTT TCC ACA GCT ACA 4998
Arg Val Tyr Cys Val Glu Gly Thr Pro Ile Asn Phe Ser Thr Ala Thr
1640 1645 1650 1655

TCT CTA AGT GAT CTA ACA ATC GAA TCC CCT CCA AAT GAG TTA GCT GCT 5046
 Ser Leu Ser Asp Leu Thr Ile Glu Ser Pro Pro Asn Glu Leu Ala Ala
 1660 1665 1670
 GGA GAA GGA GTT AGA GGA GGA GCA CAG TCA GGT GAA TTT GAA AAA CGA 5094
 Gly Glu Gly Val Arg Gly Gly Ala Gln Ser Gly Glu Phe Glu Lys Arg
 1675 1680 1685
 GAT ACC ATT CCT ACA GAA GGC AGA AGT ACA GAT GAG GCT CAA GGA GGA 5142
 Asp Thr Ile Pro Thr Glu Gly Arg Ser Thr Asp Glu Ala Gln Gly Gly
 1690 1695 1700
 AAA ACC TCA TCT GTA ACC ATA CCT GAA TTG GAT GAC AAT AAA GCA GAG 5190
 Lys Thr Ser Ser Val Thr Ile Pro Glu Leu Asp Asp Asn Lys Ala Glu
 1705 1710 1715
 GAA GGT GAT ATT CTT GCA GAA TGC ATT AAT TCT GCT ATG CCC AAA GGG 5238
 Glu Gly Asp Ile Leu Ala Glu Cys Ile Asn Ser Ala Met Pro Lys Gly
 1720 1725 1730 1735
 AAA AGT CAC AAG CCT TTC CGT GTG AAA AAG ATA ATG GAC CAG GTC CAG 5286
 Lys Ser His Lys Pro Phe Arg Val Lys Lys Ile Met Asp Gln Val Gln
 1740 1745 1750
 CAA GCA TCT GCG TCG TCT TCT GCA CCC AAC AAA AAT CAG TTA GAT GGT 5334
 Gln Ala Ser Ala Ser Ser Ser Ala Pro Asn Lys Asn Gln Leu Asp Gly
 1755 1760 1765
 AAG AAA AAG AAA CCA ACT TCA CCA GAA AAA CCT ATA CCA CAA AAT ACT 5382
 Lys Lys Lys Lys Pro Thr Ser Pro Val Lys Pro Ile Pro Gln Asn Thr
 1770 1775 1780
 GAA TAT AGG ACA CGT GTA AGA AAA AAT GCA GAC TCA AAA AAT AAT TTA 5430
 Glu Tyr Arg Thr Arg Val Arg Lys Asn Ala Asp Ser Lys Asn Asn Leu
 1785 1790 1795
 AAT GCT GAG AGA GTT TTC TCA GAC AAG AAA GAT TCA AAG AAA CAG AAT 5478
 Asn Ala Glu Arg Val Phe Ser Asp Asn Lys Asp Ser Lys Lys Gln Asn
 1800 1805 1810 1815
 TTG AAA AAT AAT TCC AAG GAC TTC AAT GAT AAG CTC CCA AAT AAT GAA 5526
 Leu Lys Asn Asn Ser Lys Asp Phe Asn Asp Lys Leu Pro Asn Asn Glu
 1820 1825 1830
 GAT AGA GTC AGA GGA AGT TTT GCT TTT GAT TCA CCT CAT CAT TAC ACG 5574
 Asp Arg Val Arg Gly Ser Phe Ala Phe Asp Ser Pro His His Tyr Thr
 1835 1840 1845
 CCT ATT GAA GGA ACT CCT TAC TGT TTT TCA CGA AAT GAT TCT TTG AGT 5622
 Pro Ile Glu Gly Thr Pro Tyr Cys Phe Ser Arg Asn Asp Ser Leu Ser
 1850 1855 1860
 TCT CTA GAT TTT GAT GAT GAT GAT GTT GAC CTT TCC AGG GAA AAG GCT 5670
 Ser Leu Asp Phe Asp Asp Asp Asp Val Asp Leu Ser Arg Glu Lys Ala
 1865 1870 1875

GAA TTA AGA AAG GCA AAA GAA AAT AAG GAA TCA GAG GCT AAA GTT ACC 5718
 Glu Leu Arg Lys Ala Lys Glu Asn Lys Glu Ser Glu Ala Lys Val Thr
 1880 1885 1890 1895
 AGC CAC ACA GAA CTA ACC TCC AAC CAA CAA TCA GCT AAT AAG ACA CAA 5766
 Ser His Thr Glu Leu Thr Ser Asn Gln Gln Ser Ala Asn Lys Thr Gln
 1900 1905 1910
 GCT ATT GCA AAG CAG CCA ATA AAT CGA GGT CAG CCT AAA CCC ATA CTT 5814
 Ala Ile Ala Lys Gln Pro Ile Asn Arg Gly Gln Pro Lys Pro Ile Leu
 1915 1920 1925
 CAG AAA CAA TCC ACT TTT CCC CAG TCA TCC AAA GAC ATA CCA GAC AGA 5862
 Gln Lys Gln Ser Thr Phe Pro Gln Ser Ser Lys Asp Ile Pro Asp Arg
 1930 1935 1940
 GGG GCA GCA ACT GAT GAA AAG TTA CAG AAT TTT GCT ATT GAA AAT ACT 5910
 Gly Ala Ala Thr Asp Glu Lys Leu Gln Asn Phe Ala Ile Glu Asn Thr
 1945 1950 1955
 CCA GTT TGC TTT TCT CAT AAT TCC TCT CTG AGT TCT CTC AGT GAC ATT 5958
 Pro Val Cys Phe Ser His Asn Ser Ser Leu Ser Ser Leu Ser Asp Ile
 1960 1965 1970 1975
 GAC CAA GAA AAC AAC AAT AAA GAA AAT GAA CCT ATC AAA GAG ACT GAG 6006
 Asp Gln Glu Asn Asn Asn Lys Glu Asn Glu Pro Ile Lys Glu Thr Glu
 1980 1985 1990
 CCC CCT GAC TCA CAG GGA GAA CCA AGT AAA CCT CAA GCA TCA GGC TAT 6054
 Pro Pro Asp Ser Gln Gly Glu Pro Ser Lys Pro Gln Ala Ser Gly Tyr
 1995 2000 2005
 GCT CCT AAA TCA TTT CAT GTT GAA GAT ACC CCA GTT TGT TTC TCA AGA 6102
 Ala Pro Lys Ser Phe His Val Glu Asp Thr Pro Val Cys Phe Ser Arg
 2010 2015 2020
 AAC AGT TCT CTC AGT TCT CTT AGT ATT GAC TCT GAA GAT GAC CTG TTG 6150
 Asn Ser Ser Leu Ser Ser Leu Ser Ile Asp Ser Glu Asp Asp Leu Leu
 2025 2030 2035
 CAG GAA TGT ATA AGC TCC GCA ATG CCA AAA AAG AAA AAG CCT TCA AGA 6198
 Gln Glu Cys Ile Ser Ser Ala Met Pro Lys Lys Lys Lys Pro Ser Arg
 2040 2045 2050 2055
 CTC AAG GGT GAT AAT GAA AAA CAT AGT CCC AGA AAT ATG GGT GGC ATA 6246
 Leu Lys Gly Asp Asn Glu Lys His Ser Pro Arg Asn Met Gly Gly Ile
 2060 2065 2070
 TTA GGT GAA GAT CTG ACA CTT GAT TTG AAA GAT ATA CAG AGA CCA GAT 6294
 Leu Gly Glu Asp Leu Thr Leu Asp Leu Lys Asp Ile Gln Arg Pro Asp
 2075 2080 2085
 TCA GAA CAT GGT CTA TCC CCT GAT TCA GAA AAT TTT GAT TGG AAA GCT 6342
 Ser Glu His Gly Leu Ser Pro Asp Ser Glu Asn Phe Asp Trp Lys Ala
 2090 2095 2100

ATT CAG GAA GGT GCA AAT TCC ATA GTA AGT AGT TTA CAT CAA GCT GCT 6390
 Ile Gln Glu Gly Ala Asn Ser Ile Val Ser Ser Leu His Gln Ala Ala
 2105 2110 2115

GCT GCT GCA TGT TTA TCT AGA CAA GCT TCG TCT GAT TCA GAT TCC ATC 6438
 Ala Ala Ala Cys Leu Ser Arg Gln Ala Ser Ser Asp Ser Asp Ser Ile
 2120 2125 2130 2135

CTT TCC CTG AAA TCA GGA ATC TCT CTG GGA TCA CCA TTT CAT CTT ACA 6486
 Leu Ser Leu Lys Ser Gly Ile Ser Leu Gly Ser Pro Phe His Leu Thr
 2140 2145 2150

CCT GAT CAA GAA GAA AAA CCC TTT ACA AGT AAT AAA GGC CCA CGA ATT 6534
 Pro Asp Gln Glu Glu Lys Pro Phe Thr Ser Asn Lys Gly Pro Arg Ile
 2155 2160 2165

CTA AAA CCA GGG GAG AAA AGT ACA TTG GAA ACT AAA AAG ATA GAA TCT 6582
 Leu Lys Pro Gly Glu Lys Ser Thr Leu Glu Thr Lys Lys Ile Glu Ser
 2170 2175 2180

GAA AGT AAA GGA ATC AAA GGA GGA AAA AAA GTT TAT AAA AGT TTG ATT 6630
 Glu Ser Lys Gly Ile Lys Gly Gly Lys Lys Val Tyr Lys Ser Leu Ile
 2185 2190 2195

ACT GGA AAA GTT CGA TCT AAT TCA GAA ATT TCA GGC CAA ATG AAA CAG 6678
 Thr Gly Lys Val Arg Ser Asn Ser Glu Ile Ser Gly Gln Met Lys Gln
 2200 2205 2210 2215

CCC CTT CAA GCA AAC ATG CCT TCA ATC TCT CGA GGC AGG ACA ATG ATT 6726
 Pro Leu Gln Ala Asn Met Pro Ser Ile Ser Arg Gly Arg Thr Met Ile
 2220 2225 2230

CAT ATT CCA GGA GTT CGA AAT AGC TCC TCA AGT ACA AGT CCT GTT TCT 6774
 His Ile Pro Gly Val Arg Asn Ser Ser Ser Ser Thr Ser Pro Val Ser
 2235 2240 2245

AAA AAA GGC CCA CCC CTT AAG ACT CCA GCC TCC AAA AGC CCT AGT GAA 6822
 Lys Lys Gly Pro Pro Leu Lys Thr Pro Ala Ser Lys Ser Pro Ser Glu
 2250 2255 2260

GGT CAA ACA GCC ACC ACT TCT CCT AGA GGA GCC AAG CCA TCT GTG AAA 6870
 Gly Gln Thr Ala Thr Thr Ser Pro Arg Gly Ala Lys Pro Ser Val Lys
 2265 2270 2275

TCA GAA TTA AGC CCT GTT GCC AGG CAG ACA TCC CAA ATA GGT GGG TCA 6918
 Ser Glu Leu Ser Pro Val Ala Arg Gln Thr Ser Gln Ile Gly Gly Ser
 2280 2285 2290 2295

AGT AAA GCA CCT TCT AGA TCA GGA TCT AGA GAT TCG ACC CCT TCA AGA 6966
 Ser Lys Ala Pro Ser Arg Ser Gly Ser Arg Asp Ser Thr Pro Ser Arg
 2300 2305 2310

CCT GCC CAG CAA CCA TTA AGT AGA CCT ATA CAG TCT CCT GGC CGA AAC 7014
 Pro Ala Gln Gln Pro Leu Ser Arg Pro Ile Gln Ser Pro Gly Arg Asn
 2315 2320 2325

TCA ATT TCC CCT GGT AGA AAT GGA ATA AGT CCT CCT AAC AAA TTA TCT 7062
 Ser Ile Ser Pro Gly Arg Asn Gly Ile Ser Pro Pro Asn Lys Leu Ser
 2330 2335 2340
 CAA CTT CCA AGG ACA TCA TCC CCT AGT ACT GCT TCA ACT AAG TCC TCA 7110
 Gln Leu Pro Arg Thr Ser Ser Pro Ser Thr Ala Ser Thr Lys Ser Ser
 2345 2350 2355
 GGT TCT GGA AAA ATG TCA TAT ACA TCT CCA GGT AGA CAG ATG AGC CAA 7158
 Gly Ser Gly Lys Met Ser Tyr Thr Ser Pro Gly Arg Gln Met Ser Gln
 2360 2365 2370 2375
 CAG AAC CTT ACC AAA CAA ACA GGT TTA TCC AAG AAT GCC AGT AGT ATT 7206
 Gln Asn Leu Thr Lys Gln Thr Gly Leu Ser Lys Asn Ala Ser Ser Ile
 2380 2385 2390
 CCA AGA AGT GAG TCT GCC TCC AAA GGA CTA AAT CAG ATG AAT AAT GGT 7254
 Pro Arg Ser Glu Ser Ala Ser Lys Gly Leu Asn Gln Met Asn Asn Gly
 2395 2400 2405
 AAT GGA GCC AAT AAA AAG GTA GAA CTT TCT AGA ATG TCT TCA ACT AAA 7302
 Asn Gly Ala Asn Lys Lys Val Glu Leu Ser Arg Met Ser Ser Thr Lys
 2410 2415 2420
 TCA AGT GGA AGT GAA TCT GAT AGA TCA GAA AGA CCT GTA TTA GTA CGC 7350
 Ser Ser Gly Ser Glu Ser Asp Arg Ser Glu Arg Pro Val Leu Val Arg
 2425 2430 2435
 CAG TCA ACT TTC ATC AAA GAA GCT CCA AGC CCA ACC TTA AGA AGA AAA 7398
 Gln Ser Thr Phe Ile Lys Glu Ala Pro Ser Pro Thr Leu Arg Arg Lys
 2440 2445 2450 2455
 TTG GAG GAA TCT GCT TCA TTT GAA TCT CTT TCT CCA TCA TCT AGA CCA 7446
 Leu Glu Glu Ser Ala Ser Phe Glu Ser Leu Ser Pro Ser Ser Arg Pro
 2460 2465 2470
 GCT TCT CCC ACT AGG TCC CAG GCA CAA ACT CCA GTT TTA AGT CCT TCC 7494
 Ala Ser Pro Thr Arg Ser Gln Ala Gln Thr Pro Val Leu Ser Pro Ser
 2475 2480 2485
 CTT CCT GAT ATG TCT CTA TCC ACA CAT TCG TCT GTT CAG GCT GGT GGA 7542
 Leu Pro Asp Met Ser Leu Ser Thr His Ser Ser Val Gln Ala Gly Gly
 2490 2495 2500
 TGG CGA AAA CTC CCA CCT AAT CTC AGT CCC ACT ATA GAG TAT AAT GAT 7590
 Trp Arg Lys Leu Pro Pro Asn Leu Ser Pro Thr Ile Glu Tyr Asn Asp
 2505 2510 2515
 GGA AGA CCA GCA AAG CGC CAT GAT ATT GCA CCG TCT CAT TCT GAA AGT 7638
 Gly Arg Pro Ala Lys Arg His Asp Ile Ala Arg Ser His Ser Glu Ser
 2520 2525 2530 2535
 CCT TCT AGA CTT CCA ATC AAT AGG TCA GGA ACC TGG AAA CGT GAG CAC 7686
 Pro Ser Arg Leu Pro Ile Asn Arg Ser Gly Thr Trp Lys Arg Glu His
 2540 2545 2550

AGC AAA CAT TCA TCA TCC CTT CCT CGA GTA AGC ACT TGG AGA AGA ACT 7734
 Ser Lys His Ser Ser Ser Leu Pro Arg Val Ser Thr Trp Arg Arg Thr
 2555 2560 2565
 GGA AGT TCA TCT TCA ATT CTT TCT GCT TCA TCA GAA TCC AGT GAA AAA 7782
 Gly Ser Ser Ser Ser Ile Leu Ser Ala Ser Ser Glu Ser Ser Glu Lys
 2570 2575 2580
 GCA AAA AGT GAG GAT GAA AAA CAT GTG AAC TCT ATT TCA GGA ACC AAA 7830
 Ala Lys Ser Glu Asp Glu Lys His Val Asn Ser Ile Ser Gly Thr Lys
 2585 2590 2595
 CAA AGT AAA GAA AAC CAA GTA TCC GCA AAA GGA ACA TGG AGA AAA ATA 7878
 Gln Ser Lys Glu Asn Gln Val Ser Ala Lys Gly Thr Trp Arg Lys Ile
 2600 2605 2610 2615
 AAA GAA AAT GAA TTT TCT CCC ACA AAT AGT ACT TCT CAG ACC GTT TCC 7926
 Lys Glu Asn Glu Phe Ser Pro Thr Asn Ser Thr Ser Gln Thr Val Ser
 2620 2625 2630
 TCA GGT GCT ACA AAT GGT GCT GAA TCA AAG ACT CTA ATT TAT CAA ATG 7974
 Ser Gly Ala Thr Asn Gly Ala Glu Ser Lys Thr Leu Ile Tyr Gln Met
 2635 2640 2645
 GCA CCT GCT GTT TCT AAA ACA GAG GAT GTT TGG GTG AGA ATT GAG GAC 8022
 Ala Pro Ala Val Ser Lys Thr Glu Asp Val Trp Val Arg Ile Glu Asp
 2650 2655 2660
 TGT CCC ATT AAC AAT CCT AGA TCT GGA AGA TCT CCC ACA GGT AAT ACT 8070
 Cys Pro Ile Asn Asn Pro Arg Ser Gly Arg Ser Pro Thr Gly Asn Thr
 2665 2670 2675
 CCC CCG GTG ATT GAC AGT GTT TCA GAA AAG GCA AAT CCA AAC ATT AAA 8118
 Pro Pro Val Ile Asp Ser Val Ser Glu Lys Ala Asn Pro Asn Ile Lys
 2680 2685 2690 2695
 GAT TCA AAA GAT AAT CAG GCA AAA CAA AAT GTG GGT AAT GGC AGT GTT 8166
 Asp Ser Lys Asp Asn Gln Ala Lys Gln Asn Val Gly Asn Gly Ser Val
 2700 2705 2710
 CCC ATG CGT ACC GTG GGT TTG GAA AAT CGC CTG ACC TCC TTT ATT CAG 8214
 Pro Met Arg Thr Val Gly Leu Glu Asn Arg Leu Thr Ser Phe Ile Gln
 2715 2720 2725
 GTG GAT GCC CCT GAC CAA AAA GGA ACT GAG ATA AAA CCA GGA CAA AAT 8262
 Val Asp Ala Pro Asp Gln Lys Gly Thr Glu Ile Lys Pro Gly Gln Asn
 2730 2735 2740
 AAT CCT GTC CCT GTA TCA GAG ACT AAT GAA AGT CCT ATA GTG GAA CGT 8310
 Asn Pro Val Pro Val Ser Glu Thr Asn Glu Ser Pro Ile Val Glu Arg
 2745 2750 2755
 ACC CCA TTC AGT TCT AGC AGC TCA AGC AAA CAC AGT TCA CCT AGT GGG 8358
 Thr Pro Phe Ser Ser Ser Ser Ser Lys His Ser Ser Pro Ser Gly
 2760 2765 2770 2775

ACT GTT GCT GCC AGA GTG ACT CCT TTT AAT TAC AAC CCA AGC CCT AGG 8406
 Thr Val Ala Ala Arg Val Thr Pro Phe Asn Tyr Asn Pro Ser Pro Arg 2790
 2780 2785
 AAA AGC AGC GCA GAT AGC ACT TCA GCT CGG CCA TCT CAG ATC CCA ACT 8454
 Lys Ser Ser Ala Asp Ser Thr Ser Ala Arg Pro Ser Gln Ile Pro Thr 2805
 2795 2800
 CCA GTG AAT AAC AAC ACA AAG AAG CGA GAT TCC AAA ACT GAC AGC ACA 8502
 Pro Val Asn Asn Asn Thr Lys Lys Arg Asp Ser Lys Thr Asp Ser Thr 2820
 2810 2815
 GAA TCC AGT GGA ACC CAA AGT CCT AAG CGC CAT TCT GGG TCT TAC CTT 8550
 Glu Ser Ser Gly Thr Gln Ser Pro Lys Arg His Ser Gly Ser Tyr Leu 2835
 2825 2830
 GTG ACA TCT GTT TAAAAGAGAG GAAGAATGAA ACTAAGAAAA TTCTATGTTA 8602
 Val Thr Ser Val 2840
 ATTACAACCTG CTATATAGAC ATTTTGTTC AAATGAACT TTAAAAGACT GAAAAATTTT 8662
 GTAAATAGGT TTGATTCTTG TTAGAGGGTT TTTGTTCTGG AAGCCATATT TGATAGTATA 8722
 CTTTGTCTTC ACTGGTCTTA TTTTGGGAGG CACTCTTGAT GGTTAGGAAA AAATAGAAAG 8782
 CCAAGTATGT TTGTACAGTA TGTTTTACAT GTATTTAAAG TAGCATCCCA TCCCAACTTC 8842
 CTTAATTATT GCTTGTCTAA AATAATGAAC ACTACAGATA GGAAATATGA TATATTGCTG 8902
 TTATCAATCA TTTCTAGATT ATAACTGAC TAACTTACA TCAGGGGAAA ATTGGTATTT 8962
 ATGCAAAAAA AAAATGTTTT TGTCCTTGTG AGTCCATCTA ACATCATAAT TAATCATGTG 9022
 GCTGTGAAAT TCACAGTAAT ATGGTTCCCG ATGAACAAAT TTACCCAGCC TGCTTTGCTT 9082
 ACTGCATGAA TGAACTGAT GGTTCAATTT CAGAAGTAAT GATTACAGT TATGTGGTCA 9142
 CATGATGTGC ATAGAGATAG CTACAGTGTA ATAATTTACA CTATTTTGTG CTCCAAACAA 9202
 AACAAAAATC TGTGTAACCTG TAAAACATTG AATGAACTA TTTTACCTGA ACTAGATTTT 9262
 ATCTGAAAGT AGGTAGAATT TTTGCTATGC TGTAATTTGT TGTATATTCT GGTATTTGAG 9322
 GTGAGATGGC TGCTCTTTAT TAATGAGACA TGAATTGTGT CTCAACAGAA ACTAAATGAA 9382
 CATTTCAGAA TAAATTATTG CTGTATGTAA ACTGTTACTG AAATTGGTAT TTGTTTGAAG 9442
 GGTGTGTTTC ACATTTGTAT TAATTAATTG TTTAAATGC CTCTTTTAAA AGCTTATATA 9502
 AATTTTTTCT TCAGCTTCTA TGCATTAAGA GTAAATTC TCTTACTGTA ATAAAAACAT 9562
 TGAAGAAGAC TGTTGCCACT TAACCATTCC ATGCGTTGGC ACTT 9606

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2843 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ala Ala Ser Tyr Asp Gln Leu Leu Lys Gln Val Glu Ala Leu
1 5 10 15
Lys Met Glu Asn Ser Asn Leu Arg Gln Glu Leu Glu Asp Asn Ser Asn
20 25 30
His Leu Thr Lys Leu Glu Thr Glu Ala Ser Asn Met Lys Glu Val Leu
35 40 45
Lys Gln Leu Gln Gly Ser Ile Glu Asp Glu Ala Met Ala Ser Ser Gly
50 55 60
Gln Ile Asp Leu Leu Glu Arg Leu Lys Glu Leu Asn Leu Asp Ser Ser
65 70 75 80
Asn Phe Pro Gly Val Lys Leu Arg Ser Lys Met Ser Leu Arg Ser Tyr
85 90 95
Gly Ser Arg Glu Gly Ser Val Ser Ser Arg Ser Gly Glu Cys Ser Pro
100 105 110
Val Pro Met Gly Ser Phe Pro Arg Arg Gly Phe Val Asn Gly Ser Arg
115 120 125
Glu Ser Thr Gly Tyr Leu Glu Glu Leu Glu Lys Glu Arg Ser Leu Leu
130 135 140
Leu Ala Asp Leu Asp Lys Glu Glu Lys Glu Lys Asp Trp Tyr Tyr Ala
145 150 155 160
Gln Leu Gln Asn Leu Thr Lys Arg Ile Asp Ser Leu Pro Leu Thr Glu
165 170 175
Asn Phe Ser Leu Gln Thr Asp Leu Thr Arg Arg Gln Leu Glu Tyr Glu
180 185 190
Ala Arg Gln Ile Arg Val Ala Met Glu Glu Gln Leu Gly Thr Cys Gln
195 200 205
Asp Met Glu Lys Arg Ala Gln Arg Arg Ile Ala Arg Ile Gln Gln Ile
210 215 220
Glu Lys Asp Ile Leu Arg Ile Arg Gln Leu Leu Gln Ser Gln Ala Thr
225 230 235 240

Glu Ala Glu Arg Ser Ser Gln Asn Lys His Glu Thr Gly Ser His Asp
 245 250 255
 Ala Glu Arg Gln Asn Glu Gly Gln Gly Val Gly Glu Ile Asn Met Ala
 260 265 270
 Thr Ser Gly Asn Gly Gln Gly Ser Thr Thr Arg Met Asp His Glu Thr
 275 280 285
 Ala Ser Val Leu Ser Ser Ser Ser Thr His Ser Ala Pro Arg Arg Leu
 290 295 300
 Thr Ser His Leu Gly Thr Lys Val Glu Met Val Tyr Ser Leu Leu Ser
 305 310 315 320
 Met Leu Gly Thr His Asp Lys Asp Asp Met Ser Arg Thr Leu Leu Ala
 325 330 335
 Met Ser Ser Ser Gln Asp Ser Cys Ile Ser Met Arg Gln Ser Gly Cys
 340 345 350
 Leu Pro Leu Leu Ile Gln Leu Leu His Gly Asn Asp Lys Asp Ser Val
 355 360 365
 Leu Leu Gly Asn Ser Arg Gly Ser Lys Glu Ala Arg Ala Arg Ala Ser
 370 375 380
 Ala Ala Leu His Asn Ile Ile His Ser Gln Pro Asp Asp Lys Arg Gly
 385 390 395 400
 Arg Arg Glu Ile Arg Val Leu His Leu Leu Glu Gln Ile Arg Ala Tyr
 405 410 415
 Cys Glu Thr Cys Trp Glu Trp Gln Glu Ala His Glu Pro Gly Met Asp
 420 425 430
 Gln Asp Lys Asn Pro Met Pro Ala Pro Val Glu His Gln Ile Cys Pro
 435 440 445
 Ala Val Cys Val Leu Met Lys Leu Ser Phe Asp Glu Glu His Arg His
 450 455 460
 Ala Met Asn Glu Leu Gly Gly Leu Gln Ala Ile Ala Glu Leu Leu Gln
 465 470 475 480
 Val Asp Cys Glu Met Tyr Gly Leu Thr Asn Asp His Tyr Ser Ile Thr
 485 490 495
 Leu Arg Arg Tyr Ala Gly Met Ala Leu Thr Asn Leu Thr Phe Gly Asp
 500 505 510
 Val Ala Asn Lys Ala Thr Leu Cys Ser Met Lys Gly Cys Met Arg Ala
 515 520 525
 Leu Val Ala Gln Leu Lys Ser Glu Ser Glu Asp Leu Gln Gln Val Ile

RR

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530 535 540
Ala Ser Val Leu Arg Asn Leu Ser Trp Arg Ala Asp Val Asn Ser Lys 560
545 550 555
Lys Thr Leu Arg Glu Val Gly Ser Val Lys Ala Leu Met Glu Cys Ala 575
565 570
Leu Glu Val Lys Lys Glu Ser Thr Leu Lys Ser Val Leu Ser Ala Leu 590
580 585
Trp Asn Leu Ser Ala His Cys Thr Glu Asn Lys Ala Asp Ile Cys Ala 605
595 600
Val Asp Gly Ala Leu Ala Phe Leu Val Gly Thr Leu Thr Tyr Arg Ser 620
610 615
Gln Thr Asn Thr Leu Ala Ile Ile Glu Ser Gly Gly Gly Ile Leu Arg 640
625 630 635
Asn Val Ser Ser Leu Ile Ala Thr Asn Glu Asp His Arg Gln Ile Leu 655
645 650
Arg Glu Asn Asn Cys Leu Gln Thr Leu Leu Gln His Leu Lys Ser His 670
660 665
Ser Leu Thr Ile Val Ser Asn Ala Cys Gly Thr Leu Trp Asn Leu Ser 685
675 680
Ala Arg Asn Pro Lys Asp Gln Glu Ala Leu Trp Asp Met Gly Ala Val 700
690 695
Ser Met Leu Lys Asn Leu Ile His Ser Lys His Lys Met Ile Ala Met 720
705 710 715
Gly Ser Ala Ala Ala Leu Arg Asn Leu Met Ala Asn Arg Pro Ala Lys 735
725 730
Tyr Lys Asp Ala Asn Ile Met Ser Pro Gly Ser Ser Leu Pro Ser Leu 750
740 745
His Val Arg Lys Gln Lys Ala Leu Glu Ala Glu Leu Asp Ala Gln His 765
755 760
Leu Ser Glu Thr Phe Asp Asn Ile Asp Asn Leu Ser Pro Lys Ala Ser 780
770 775
His Arg Ser Lys Gln Arg His Lys Gln Ser Leu Tyr Gly Asp Tyr Val 800
785 790 795
Phe Asp Thr Asn Arg His Asp Asp Asn Arg Ser Asp Asn Phe Asn Thr 815
805 810
Gly Asn Met Thr Val Leu Ser Pro Tyr Leu Asn Thr Thr Val Leu Pro

820

825

830

Ser Ser Ser Ser Ser Arg Gly Ser Leu Asp Ser Ser Arg Ser Glu Lys
835 840 845

Asp Arg Ser Leu Glu Arg Glu Arg Gly Ile Gly Leu Gly Asn Tyr His
850 855 860

Pro Ala Thr Glu Asn Pro Gly Thr Ser Ser Lys Arg Gly Leu Gln Ile
865 870 875 880

Ser Thr Thr Ala Ala Gln Ile Ala Lys Val Met Glu Glu Val Ser Ala
885 890 895

Ile His Thr Ser Gln Glu Asp Arg Ser Ser Gly Ser Thr Thr Glu Leu
900 905 910

His Cys Val Thr Asp Glu Arg Asn Ala Leu Arg Arg Ser Ser Ala Ala
915 920 925

His Thr His Ser Asn Thr Tyr Asn Phe Thr Lys Ser Glu Asn Ser Asn
930 935 940

Arg Thr Cys Ser Met Pro Tyr Ala Lys Leu Glu Tyr Lys Arg Ser Ser
945 950 955 960

Asn Asp Ser Leu Asn Ser Val Ser Ser Asn Asp Gly Tyr Gly Lys Arg
965 970 975

Gly Gln Met Lys Pro Ser Ile Glu Ser Tyr Ser Glu Asp Asp Glu Ser
980 985 990

Lys Phe Cys Ser Tyr Gly Gln Tyr Pro Ala Asp Leu Ala His Lys Ile
995 1000 1005

His Ser Ala Asn His Met Asp Asp Asn Asp Gly Glu Leu Asp Thr Pro
1010 1015 1020

Ile Asn Tyr Ser Leu Lys Tyr Ser Asp Glu Gln Leu Asn Ser Gly Arg
1025 1030 1035 1040

Gln Ser Pro Ser Gln Asn Glu Arg Trp Ala Arg Pro Lys His Ile Ile
1045 1050 1055

Glu Asp Glu Ile Lys Gln Ser Glu Gln Arg Gln Ser Arg Asn Gln Ser
1060 1065 1070

Thr Thr Tyr Pro Val Tyr Thr Glu Ser Thr Asp Asp Lys His Leu Lys
1075 1080 1085

Phe Gln Pro His Phe Gly Gln Gln Glu Cys Val Ser Pro Tyr Arg Ser
1090 1095 1100

Arg Gly Ala Asn Gly Ser Glu Thr Asn Arg Val Gly Ser Asn His Gly

SECRET - 11899

H714

1105 1110 1115 1120
 Ile Asn Gln Asn Val Ser Gln Ser Leu Cys Gln Glu Asp Asp Tyr Glu
 1125 1130 1135
 Asp Asp Lys Pro Thr Asn Tyr Ser Glu Arg Tyr Ser Glu Glu Glu Gln
 1140 1145 1150
 His Glu Glu Glu Glu Arg Pro Thr Asn Tyr Ser Ile Lys Tyr Asn Glu
 1155 1160 1165
 Glu Lys Arg His Val Asp Gln Pro Ile Asp Tyr Ser Leu Lys Tyr Ala
 1170 1175 1180
 Thr Asp Ile Pro Ser Ser Gln Lys Gln Ser Phe Ser Phe Ser Lys Ser
 1185 1190 1195 1200
 Ser Ser Gly Gln Ser Ser Lys Thr Glu His Met Ser Ser Ser Ser Glu
 1205 1210 1215
 Asn Thr Ser Thr Pro Ser Ser Asn Ala Lys Arg Gln Asn Gln Leu His
 1220 1225 1230
 Pro Ser Ser Ala Gln Ser Arg Ser Gly Gln Pro Gln Lys Ala Ala Thr
 1235 1240 1245
 Cys Lys Val Ser Ser Ile Asn Gln Glu Thr Ile Gln Thr Tyr Cys Val
 1250 1255 1260
 Glu Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu Ser Ser Leu
 1265 1270 1275 1280
 Ser Ser Ala Glu Asp Glu Ile Gly Cys Asn Gln Thr Thr Gln Glu Ala
 1285 1290 1295
 Asp Ser Ala Asn Thr Leu Gln Ile Ala Glu Ile Lys Gly Lys Ile Gly
 1300 1305 1310
 Thr Arg Ser Ala Glu Asp Pro Val Ser Glu Val Pro Ala Val Ser Gln
 1315 1320 1325
 His Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser
 1330 1335 1340
 Glu Ser Ala Arg His Lys Ala Val Glu Phe Pro Ser Gly Ala Lys Ser
 1345 1350 1355 1360
 Pro Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr
 1365 1370 1375
 Val Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser
 1380 1385 1390
 Leu Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu

1395 1400 1405
 Pro Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro
 1410 1415 1420
 Asp Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro
 1425 1430 1435 1440
 Pro Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys
 1445 1450 1455
 Ala Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val
 1460 1465 1470
 Asn Ala Ala Val Gln Arg Val Gln Val Leu Pro Asp Ala Asp Thr Leu
 1475 1480 1485
 Leu His Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser
 1490 1495 1500
 Ser Leu Ser Ala Leu Ser Leu Asp Glu Pro Phe Ile Gln Lys Asp Val
 1505 1510 1515 1520
 Glu Leu Arg Ile Met Pro Pro Val Gln Glu Asn Asp Asn Gly Asn Glu
 1525 1530 1535
 Thr Glu Ser Glu Gln Pro Lys Glu Ser Asn Glu Asn Gln Glu Lys Glu
 1540 1545 1550
 Ala Glu Lys Thr Ile Asp Ser Glu Lys Asp Leu Leu Asp Asp Ser Asp
 1555 1560 1565
 Asp Asp Asp Ile Glu Ile Leu Glu Glu Cys Ile Ile Ser Ala Met Pro
 1570 1575 1580
 Thr Lys Ser Ser Arg Lys Gly Lys Lys Pro Ala Gln Thr Ala Ser Lys
 1585 1590 1595 1600
 Leu Pro Pro Pro Val Ala Arg Lys Pro Ser Gln Leu Pro Val Tyr Lys
 1605 1610 1615
 Leu Leu Pro Ser Gln Asn Arg Leu Gln Pro Gln Lys His Val Ser Phe
 1620 1625 1630
 Thr Pro Gly Asp Asp Met Pro Arg Val Tyr Cys Val Glu Gly Thr Pro
 1635 1640 1645
 Ile Asn Phe Ser Thr Ala Thr Ser Leu Ser Asp Leu Thr Ile Glu Ser
 1650 1655 1660
 Pro Pro Asn Glu Leu Ala Ala Gly Glu Gly Val Arg Gly Gly Ala Gln
 1665 1670 1675 1680
 Ser Gly Glu Phe Glu Lys Arg Asp Thr Ile Pro Thr Glu Gly Arg Ser

AA14

SECRET - 6842460

1685 1690 1695
 Thr Asp Glu Ala Gln Gly Gly Lys Thr Ser Ser Val Thr Ile Pro Glu
 1700 1705 1710
 Leu Asp Asp Asn Lys Ala Glu Glu Gly Asp Ile Leu Ala Glu Cys Ile
 1715 1720 1725
 Asn Ser Ala Met Pro Lys Gly Lys Ser His Lys Pro Phe Arg Val Lys
 1730 1735 1740
 Lys Ile Met Asp Gln Val Gln Gln Ala Ser Ala Ser Ser Ala Pro
 1745 1750 1755 1760
 Asn Lys Asn Gln Leu Asp Gly Lys Lys Lys Lys Pro Thr Ser Pro Val
 1765 1770 1775
 Lys Pro Ile Pro Gln Asn Thr Glu Tyr Arg Thr Arg Val Arg Lys Asn
 1780 1785 1790
 Ala Asp Ser Lys Asn Asn Leu Asn Ala Glu Arg Val Phe Ser Asp Asn
 1795 1800 1805
 Lys Asp Ser Lys Lys Gln Asn Leu Lys Asn Asn Ser Lys Asp Phe Asn
 1810 1815 1820
 Asp Lys Leu Pro Asn Asn Glu Asp Arg Val Arg Gly Ser Phe Ala Phe
 1825 1830 1835 1840
 Asp Ser Pro His His Tyr Thr Pro Ile Glu Gly Thr Pro Tyr Cys Phe
 1845 1850 1855
 Ser Arg Asn Asp Ser Leu Ser Ser Leu Asp Phe Asp Asp Asp Val
 1860 1865 1870
 Asp Leu Ser Arg Glu Lys Ala Glu Leu Arg Lys Ala Lys Glu Asn Lys
 1875 1880 1885
 Glu Ser Glu Ala Lys Val Thr Ser His Thr Glu Leu Thr Ser Asn Gln
 1890 1895 1900
 Gln Ser Ala Asn Lys Thr Gln Ala Ile Ala Lys Gln Pro Ile Asn Arg
 1905 1910 1915 1920
 Gly Gln Pro Lys Pro Ile Leu Gln Lys Gln Ser Thr Phe Pro Gln Ser
 1925 1930 1935
 Ser Lys Asp Ile Pro Asp Arg Gly Ala Ala Thr Asp Glu Lys Leu Gln
 1940 1945 1950
 Asn Phe Ala Ile Glu Asn Thr Pro Val Cys Phe Ser His Asn Ser Ser
 1955 1960 1965
 Leu Ser Ser Leu Ser Asp Ile Asp Gln Glu Asn Asn Asn Lys Glu Asn
 1970 1975 1980

Glu Pro Ile Lys Glu Thr Glu Pro Pro Asp Ser Gln Gly Glu Pro Ser
 1985 1990 1995 2000
 Lys Pro Gln Ala Ser Gly Tyr Ala Pro Lys Ser Phe His Val Glu Asp
 2005 2010 2015
 Thr Pro Val Cys Phe Ser Arg Asn Ser Ser Leu Ser Ser Leu Ser Ile
 2020 2025 2030
 Asp Ser Glu Asp Asp Leu Leu Gln Glu Cys Ile Ser Ser Ala Met Pro
 2035 2040 2045
 Lys Lys Lys Lys Pro Ser Arg Leu Lys Gly Asp Asn Glu Lys His Ser
 2050 2055 2060
 Pro Arg Asn Met Gly Gly Ile Leu Gly Glu Asp Leu Thr Leu Asp Leu
 2065 2070 2075 2080
 Lys Asp Ile Gln Arg Pro Asp Ser Glu His Gly Leu Ser Pro Asp Ser
 2085 2090 2095
 Glu Asn Phe Asp Trp Lys Ala Ile Gln Glu Gly Ala Asn Ser Ile Val
 2100 2105 2110
 Ser Ser Leu His Gln Ala Ala Ala Ala Cys Leu Ser Arg Gln Ala
 2115 2120 2125
 Ser Ser Asp Ser Asp Ser Ile Leu Ser Leu Lys Ser Gly Ile Ser Leu
 2130 2135 2140
 Gly Ser Pro Phe His Leu Thr Pro Asp Gln Glu Glu Lys Pro Phe Thr
 2145 2150 2155 2160
 Ser Asn Lys Gly Pro Arg Ile Leu Lys Pro Gly Glu Lys Ser Thr Leu
 2165 2170 2175
 Glu Thr Lys Lys Ile Glu Ser Glu Ser Lys Gly Ile Lys Gly Gly Lys
 2180 2185 2190
 Lys Val Tyr Lys Ser Leu Ile Thr Gly Lys Val Arg Ser Asn Ser Glu
 2195 2200 2205
 Ile Ser Gly Gln Met Lys Gln Pro Leu Gln Ala Asn Met Pro Ser Ile
 2210 2215 2220
 Ser Arg Gly Arg Thr Met Ile His Ile Pro Gly Val Arg Asn Ser Ser
 2225 2230 2235 2240
 Ser Ser Thr Ser Pro Val Ser Lys Lys Gly Pro Pro Leu Lys Thr Pro
 2245 2250 2255
 Ala Ser Lys Ser Pro Ser Glu Gly Gln Thr Ala Thr Thr Ser Pro Arg
 2260 2265 2270

414A

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Gly Ala Lys Pro Ser Val Lys Ser Glu Leu Ser Pro Val Ala Arg Gln
 2275 2280 2285
 Thr Ser Gln Ile Gly Gly Ser Ser Lys Ala Pro Ser Arg Ser Gly Ser
 2290 2295 2300
 Arg Asp Ser Thr Pro Ser Arg Pro Ala Gln Gln Pro Leu Ser Arg Pro
 2305 2310 2315 2320
 Ile Gln Ser Pro Gly Arg Asn Ser Ile Ser Pro Gly Arg Asn Gly Ile
 2325 2330 2335
 Ser Pro Pro Asn Lys Leu Ser Gln Leu Pro Arg Thr Ser Ser Pro Ser
 2340 2345 2350
 Thr Ala Ser Thr Lys Ser Ser Gly Ser Gly Lys Met Ser Tyr Thr Ser
 2355 2360 2365
 Pro Gly Arg Gln Met Ser Gln Gln Asn Leu Thr Lys Gln Thr Gly Leu
 2370 2375 2380
 Ser Lys Asn Ala Ser Ser Ile Pro Arg Ser Glu Ser Ala Ser Lys Gly
 2385 2390 2395 2400
 Leu Asn Gln Met Asn Asn Gly Asn Gly Ala Asn Lys Lys Val Glu Leu
 2405 2410 2415
 Ser Arg Met Ser Ser Thr Lys Ser Ser Gly Ser Glu Ser Asp Arg Ser
 2420 2425 2430
 Glu Arg Pro Val Leu Val Arg Gln Ser Thr Phe Ile Lys Glu Ala Pro
 2435 2440 2445
 Ser Pro Thr Leu Arg Arg Lys Leu Glu Glu Ser Ala Ser Phe Glu Ser
 2450 2455 2460
 Leu Ser Pro Ser Ser Arg Pro Ala Ser Pro Thr Arg Ser Gln Ala Gln
 2465 2470 2475 2480
 Thr Pro Val Leu Ser Pro Ser Leu Pro Asp Met Ser Leu Ser Thr His
 2485 2490 2495
 Ser Ser Val Gln Ala Gly Gly Trp Arg Lys Leu Pro Pro Asn Leu Ser
 2500 2505 2510
 Pro Thr Ile Glu Tyr Asn Asp Gly Arg Pro Ala Lys Arg His Asp Ile
 2515 2520 2525
 Ala Arg Ser His Ser Glu Ser Pro Ser Arg Leu Pro Ile Asn Arg Ser
 2530 2535 2540
 Gly Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg
 2545 2550 2555 2560

Val Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ser Ile Leu Ser Ala
 2565 2570 2575
 Ser Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val
 2580 2585 2590
 Asn Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala
 2595 2600 2605
 Lys Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn
 2610 2615 2620
 Ser Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser
 2625 2630 2635 2640
 Lys Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp
 2645 2650 2655
 Val Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly
 2660 2665 2670
 Arg Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu
 2675 2680 2685
 Lys Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln
 2690 2695 2700
 Asn Val Gly Asn Gly Ser Val Pro Met Arg Thr Val Gly Leu Glu Asn
 2705 2710 2715 2720
 Arg Leu Thr Ser Phe Ile Gln Val Asp Ala Pro Asp Gln Lys Gly Thr
 2725 2730 2735
 Glu Ile Lys Pro Gly Gln Asn Asn Pro Val Pro Val Ser Glu Thr Asn
 2740 2745 2750
 Glu Ser Pro Ile Val Glu Arg Thr Pro Phe Ser Ser Ser Ser Ser
 2755 2760 2765
 Lys His Ser Ser Pro Ser Gly Thr Val Ala Ala Arg Val Thr Pro Phe
 2770 2775 2780
 Asn Tyr Asn Pro Ser Pro Arg Lys Ser Ser Ala Asp Ser Thr Ser Ala
 2785 2790 2795 2800
 Arg Pro Ser Gln Ile Pro Thr Pro Val Asn Asn Asn Thr Lys Lys Arg
 2805 2810 2815
 Asp Ser Lys Thr Asp Ser Thr Glu Ser Ser Gly Thr Gln Ser Pro Lys
 2820 2825 2830
 Arg His Ser Gly Ser Tyr Leu Val Thr Ser Val
 2835 2840

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: DP1(TB2)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCA GTC GCC GCT CCA GTC TAT CCG GCA CTA GGA ACA GCC CCG GGN GGC	48
Ala Val Ala Ala Pro Val Tyr Pro Ala Leu Gly Thr Ala Pro Gly Gly	
1 5 10 15	
GAG ACG GTC CCC GCC ATG TCT GCG GCC ATG AGG GAG AGG TTC GAC CGG	96
Glu Thr Val Pro Ala Met Ser Ala Ala Met Arg Glu Arg Phe Asp Arg	
20 25 30	
TTC CTG CAC GAG AAG AAC TGC ATG ACT GAC CTT CTG GCC AAG CTC GAG	144
Phe Leu His Glu Lys Asn Cys Met Thr Asp Leu Leu Ala Lys Leu Glu	
35 40 45	
GCC AAA ACC GGC GTG AAC AGG AGC TTC ATC GCT CTT GGT GTC ATC GGA	192
Ala Lys Thr Gly Val Asn Arg Ser Phe Ile Ala Leu Gly Val Ile Gly	
50 55 60	
CTG GTG GCC TTG TAC CTG GTG TTC GGT TAT GGA GCC TCT CTC CTC TGC	240
Leu Val Ala Leu Tyr Leu Val Phe Gly Tyr Gly Ala Ser Leu Leu Cys	
65 70 75	
AAC CTG ATA GGA TTT GGC TAC CCA GCC TAC ATC TCA ATT AAA GCT ATA	288
Asn Leu Ile Gly Phe Gly Tyr Pro Ala Tyr Ile Ser Ile Lys Ala Ile	
85 90 95	
GAG AGT CCC AAC AAA GAA GAT GAT ACC CAG TGG CTG ACC TAC TGG GTA	336
Glu Ser Pro Asn Lys Glu Asp Asp Thr Gln Trp Leu Thr Tyr Trp Val	
100 105 110	
GTG TAT GGT GTG TTC AGC ATT GCT GAA TTC TTC TCT GAT ATC TTC CTG	384
Val Tyr Gly Val Phe Ser Ile Ala Glu Phe Phe Ser Asp Ile Phe Leu	
115 120 125	
TCA TGG TTC CCC TTC TAC TAC ATG CTG AAG TGT GGC TTC CTG TTG TGG	432

Ser Trp Phe Pro Phe Tyr Tyr Met Leu Lys Cys Gly Phe Leu Leu Trp
 130 135 140

TGC ATG GCC CCG AGC CCT TCT AAT GGG GCT GAA CTG CTC TAC AAG CGC 480
 Cys Met Ala Pro Ser Pro Ser Asn Gly Ala Glu Leu Leu Tyr Lys Arg
 145 150 155 160

ATC ATC CGT CCT TTC TTC CTG AAG CAC GAG TCC CAG ATG GAC AGT GTG 528
 Ile Ile Arg Pro Phe Phe Leu Lys His Glu Ser Gln Met Asp Ser Val
 165 170 175

GTC AAG GAC CTT AAA GAC AAG TCC AAA GAG ACT GCA GAT GCC ATC ACT 576
 Val Lys Asp Leu Lys Asp Lys Ser Lys Glu Thr Ala Asp Ala Ile Thr
 180 185 190

AAA GAA GCG AAG AAA GCT ACC GTG AAT TTA CTG GGT GAA GAA AAG AAG 624
 Lys Glu Ala Lys Lys Ala Thr Val Asn Leu Leu Gly Glu Glu Lys Lys
 195 200 205

AGC ACC TAAACCAGAC TAAACCAGAC TGGATGGAAA CTCCTGCCC TCTCTGTACC 680
 Ser Thr
 210

TTCCTACTGG AGCTTGATGT TATATTAGGG ACTGTGGTAT AATTATTTTA ATAATGTTGC 740

CTTGGAAACA TTTTGTAGAT ATTAAGATT GGAATGTGTT GTAAGTTTCT TTGCTTACTT 800

TTACTGTCTA TATATATAGG GAGCACTTTA AACTTAATGC AGTGGGCAGT GTCCACGTTT 860

TTGGAAAATG TATTTTGCCT CTGGGTAGGA AAAGATGTAT GTTGCTATCC TGCAGGAAAT 920

ATAACTTAA AATAAAATTA TATACCCAC AGGCTGTGTA CTTTACTGGG CTCTCCCTGC 980

ACGSATTTTC TCTGTAGTTA CATTTAGGRT AATCTTTATG GTTCTACTTC CTRTAATGTA 1040

CAATTTTATA TAATTCNGRA ATGTTTAA TGTATTTGTG CACATGTACA TATGGAAATG 1100

TTACTGTCTG ACTACANCAT GCATCATGCT CATGGGGAGG GAGCAGGGGA AGGTTGTATG 1160

TGTCATTTAT AACTTCTGTA CAGTAAGACC ACCTGCCAAA AGCTGGAGGA ACCATTGTGC 1220

TGGTGTGGTC TACTAAATAA TACTTTAGGA AATACGTGAT TAATATGCAA GTGAACAAAG 1280

TGAGAAATGA AATCGAATGG AGATTGCGCT GCTTGTTCCT GTAGTATATG GCATATGAAT 1340

ACCAGGATAG CTTTATAAAG CAGTTAGTTA GTTAGTTACT CACTCTAGTG ATAAATCGGG 1400

AAATTTACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAG 1460

AGTACCCTGT AACTCTCAAT TCCCTGAAAA ACTAGTAATA CTGTCTTATC TGCTATAAAC 1520

TTTACATATT TGTCTATTGT CAAGATGCTA CANTGGAMNC CATTCTGGT TTTATCTTCA 1580

NAGSGGAGAN ACATGTTGAT TTAGTCTTCT TTCCCAATCT TCTTTTTTAA MCCAGTTTNA 1640

GGMNCTTCTG RAGATTTGYC CACCTCTGAT TACATGTATG TTCTYGTGTTG TATCATKAGC 1700
 AACACATGC TAATGRCGAC ACCTAGCTCT RAGMGCAATT CTGGGAGANT GARAGGNWGT 1760
 ATARAGTMNC CCATAATCTG CTTGGCAATA GTTAAGTCAA TCTATCTTCA GTTTTTCTCT 1820
 GGCCTTTAAG GTCAAACACA AGAGGCTTCC CTAGTTTACA AGTCAGAGTC ACTTGTAGTC 1880
 CATTTAAATG CCCTCATCCG TATTCTTTGT GTTGATAAGC TGCACAKGAC TACATAGTAA 1940
 GTACAGANCA GTAAAGTTAA NNCGGATGTC TCCATTGATC TGCCAANTCG NTATAGAGAG 2000
 CAATTTGTCT GGACTAGAAA ATCTGAGTTT TACACCATAC TGTTAAGAGT CCTTTTGAAT 2060
 TAAACTAGAC TAAACAAGT GTATAACTAA ACTAACAAGA TTAAATATCC AGCCAGTACA 2120
 GTATTTTTTA AGGCAAATAA AGATGATTAG CTCACCTTGA GNTAACAATC AGGTAAGATC 2180
 ATNACAATGT CTCATGATGT NAANAATATT AAAGATATCA ATACTAAGTG ACAGTATCAC 2240
 NNCTAATATA ATATGGATCA GAGCATTAT TTTGGGGAGG AAAACAGTGG TGATTACCGG 2300
 CATTTTATTA AACTTAAAC TTTGTAGAAA GCAAACAAAA TTGTTCTTGG GAGAAAATCA 2360
 ACTTTTAGAT TAAAAAATT TTAAGTAWCT AGGAGTATTT AAATCCTTTT CCCATAAATA 2420
 AAAGTACAGT TTTCTTGGTG GCAGAAATGAA AATCAGCAAC NTCTAGCATA TAGACTATAT 2480
 AATCAGATTG ACAGCATATA GAATATATTA TCAGACAAGA TGAGGAGGTA CAAAAGTTAC 2540
 TATTGCTCAT AATGACTTAC AGGCTAAAAA TAGNTNTAAA ATACTATATT AAATTCTGAA 2600
 TGCAATTTTT TTTTGTCCC TTGAGACCAA AATTAAAGTT AACTGTTGCT GGCAGTCTAA 2660
 GTGTAAATGT TAACAGCAGG AGAAGTTAAG AATTGAGCAG TTCTGTTGCA TGATTCCCA 2720
 AATGAAATAC TGCCTTGGCT AGAGTTTGAA AACTAATTG AGCCTGTGCC TGGCTAGAAA 2780
 ACAAGCGTTT ATTTGAATGT GAATAGTGTT TCAAAGGTAT GTAGTTACAG AATTCCTACC 2840
 AAACAGCTTA AATTCTTCAA GAAAGAATTC CTGCAGCAGT TATTCCTTA CCTGAAGGCT 2900
 TCAATCATTT GGATCAACAA CTGCTACTCT CGGGAAGACT CCTCTACTCA CAGCTGAAGA 2960
 AAATGAGCAC ACCCTTCACA CTGTTATCAC CTATCCTGAA GATGTGATAC ACTGAATGGA 3020
 AATAAATAGA TGTAATAAAA ATTGAGWTCT CATTTAAAAA AAACCATGTG CCCAATGGGA 3080
 AAATGACCTC ATGTTGTGGT TTAAACAGCA ACTGCACCCA CTAGCACAGC CCATTGAGCT 3140
 ANCCTATATA TACATCTCTG TCAGTGCCCC TC 3172

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Val Ala Ala Pro Val Tyr Pro Ala Leu Gly Thr Ala Pro Gly Gly
1 5 10 15
Glu Thr Val Pro Ala Met Ser Ala Ala Met Arg Glu Arg Phe Asp Arg
20 25 30
Phe Leu His Glu Lys Asn Cys Met Thr Asp Leu Leu Ala Lys Leu Glu
35 40 45
Ala Lys Thr Gly Val Asn Arg Ser Phe Ile Ala Leu Gly Val Ile Gly
50 55 60
Leu Val Ala Leu Tyr Leu Val Phe Gly Tyr Gly Ala Ser Leu Leu Cys
65 70 75 80
Asn Leu Ile Gly Phe Gly Tyr Pro Ala Tyr Ile Ser Ile Lys Ala Ile
85 90 95
Glu Ser Pro Asn Lys Glu Asp Asp Thr Gln Trp Leu Thr Tyr Trp Val
100 105 110
Val Tyr Gly Val Phe Ser Ile Ala Glu Phe Phe Ser Asp Ile Phe Leu
115 120 125
Ser Trp Phe Pro Phe Tyr Tyr Met Leu Lys Cys Gly Phe Leu Leu Trp
130 135 140
Cys Met Ala Pro Ser Pro Ser Asn Gly Ala Glu Leu Leu Tyr Lys Arg
145 150 155 160
Ile Ile Arg Pro Phe Phe Leu Lys His Glu Ser Gln Met Asp Ser Val
165 170 175
Val Lys Asp Leu Lys Asp Lys Ser Lys Glu Thr Ala Asp Ala Ile Thr
180 185 190
Lys Glu Ala Lys Lys Ala Thr Val Asn Leu Leu Gly Glu Glu Lys Lys
195 200 205
Ser Thr
210

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:
(B) CLONE: TB1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Val Ala Pro Val Val Val Gly Ser Gly Arg Ala Pro Arg His Pro Ala
1 5 10 15
Pro Ala Ala Met His Pro Arg Arg Pro Asp Gly Phe Asp Gly Leu Gly
20 25 30
Tyr Arg Gly Gly Ala Arg Asp Glu Gln Gly Phe Gly Gly Ala Phe Pro
35 40 45
Ala Arg Ser Phe Ser Thr Gly Ser Asp Leu Gly His Trp Val Thr Thr
50 55 60
Pro Pro Asp Ile Pro Gly Ser Arg Asn Leu His Trp Gly Glu Lys Ser
65 70 75 80
Pro Pro Tyr Gly Val Pro Thr Thr Ser Thr Pro Tyr Glu Gly Pro Thr
85 90 95
Glu Glu Pro Phe Ser Ser Gly Gly Gly Gly Ser Val Gln Gly Gln Ser
100 105 110
Ser Glu Gln Leu Asn Arg Phe Ala Gly Phe Gly Ile Gly Leu Ala Ser
115 120 125
Leu Phe Thr Glu Asn Val Leu Ala His Pro Cys Ile Val Leu Arg Arg
130 135 140
Gln Cys Gln Val Asn Tyr His Ala Gln His Tyr His Leu Thr Pro Phe
145 150 155 160
Thr Val Ile Asn Ile Met Tyr Ser Phe Asn Lys Thr Gln Gly Pro Arg
165 170 175
Ala Leu Trp Lys Gly Met Gly Ser Thr Phe Ile Val Gln Gly Val Thr
180 185 190
Leu Gly Ala Glu Gly Ile Ile Ser Glu Phe Thr Pro Leu Pro Arg Glu
195 200 205

Val Leu His Lys Trp Ser Pro Lys Gln Ile Gly Glu His Leu Leu Leu
 210 215 220
 Lys Ser Leu Thr Tyr Val Val Ala Met Pro Phe Tyr Ser Ala Ser Leu
 225 230 235 240
 Ile Glu Thr Val Gln Ser Glu Ile Ile Arg Asp Asn Thr Gly Ile Leu
 245 250 255
 Glu Cys Val Lys Glu Gly Ile Gly Arg Val Ile Gly Met Gly Val Pro
 260 265 270
 His Ser Lys Arg Leu Leu Pro Leu Leu Ser Leu Ile Phe Pro Thr Val
 275 280 285
 Leu His Gly Val Leu His Tyr Ile Ile Ser Ser Val Ile Gln Lys Phe
 290 295 300
 Val Leu Leu Ile Leu Lys Arg Lys Thr Tyr Asn Ser His Leu Ala Glu
 305 310 315 320
 Ser Thr Ser Pro Val Gln Ser Met Leu Asp Ala Tyr Phe Pro Glu Leu
 325 330 335
 Ile Ala Asn Phe Ala Ala Ser Leu Cys Ser Asp Val Ile Leu Tyr Pro
 340 345 350
 Leu Glu Thr Val Leu His Arg Leu His Ile Gln Gly Thr Arg Thr Ile
 355 360 365
 Ile Asp Asn Thr Asp Leu Gly Tyr Glu Val Leu Pro Ile Asn Thr Gln
 370 375 380
 Tyr Glu Gly Met Arg Asp Cys Ile Asn Thr Ile Arg Gln Glu Glu Gly
 385 390 395 400
 Val Phe Gly Phe Tyr Lys Gly Phe Gly Ala Val Ile Ile Gln Tyr Thr
 405 410 415
 Leu His Ala Ala Val Leu Gln Ile Thr Lys Ile Ile Tyr Ser Thr Leu
 420 425 430
 Leu Gln

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:
(B) CLONE: YS-39(TB2)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

RA 14

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Glu Leu Arg Arg Phe Asp Arg Phe Leu His Glu Lys Asn Cys Met Thr
1 5 10 15
Asp Leu Leu Ala Lys Leu Glu Ala Lys Thr Gly Val Asn Arg Ser Phe
20 25 30
Ile Ala Leu Gly Val Ile Gly Leu Val Ala Leu Tyr Leu Val Phe Gly
35 40 45
Tyr Gly Ala Ser Leu Leu Cys Asn Leu Ile Gly Phe Gly Tyr Pro Ala
50 55 60
Tyr Ile Ser Ile Lys Ala Ile Glu Ser Pro Asn Lys Glu Asp Asp Thr
65 70 75 80
Gln Trp Leu Thr Tyr Trp Val Val Tyr Gly Val Phe Ser Ile Ala Glu
85 90 95
Phe Phe Ser Asp Ile Phe Leu Ser Trp Phe Pro Phe Tyr Tyr Ile Leu
100 105 110
Lys Cys Gly Phe Leu Leu Trp Cys Met Ala Pro Ser Pro Ser Asn Gly
115 120 125
Ala Glu Leu Leu Tyr Lys Arg Ile Ile Arg Pro Phe Phe Leu Lys His
130 135 140
Glu Ser Gln Met Asp Ser Val Val Lys Asp Leu Lys Asp Lys Ala Lys
145 150 155 160
Glu Thr Ala Asp Ala Ile Thr Lys Glu Ala Lys Lys Ala Thr Val Asn
165 170 175
Leu Leu Gly Glu Glu Lys Lys Ser Thr
180 185

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2843 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:
(B) CLONE: APC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Ala Ala Ser Tyr Asp Gln Leu Leu Lys Gln Val Glu Ala Leu
1 5 10 15
Lys Met Glu Asn Ser Asn Leu Arg Gln Glu Leu Glu Asp Asn Ser Asn
20 25 30
His Leu Thr Lys Leu Glu Thr Glu Ala Ser Asn Met Lys Glu Val Leu
35 40 45
Lys Gln Leu Gln Gly Ser Ile Glu Asp Glu Ala Met Ala Ser Ser Gly
50 55 60
Gln Ile Asp Leu Leu Glu Arg Leu Lys Glu Leu Asn Leu Asp Ser Ser
65 70 75 80
Asn Phe Pro Gly Val Lys Leu Arg Ser Lys Met Ser Leu Arg Ser Tyr
85 90 95
Gly Ser Arg Glu Gly Ser Val Ser Ser Arg Ser Gly Glu Cys Ser Pro
100 105 110
Val Pro Met Gly Ser Phe Pro Arg Arg Gly Phe Val Asn Gly Ser Arg
115 120 125
Glu Ser Thr Gly Tyr Leu Glu Glu Leu Glu Lys Glu Arg Ser Leu Leu
130 135 140
Leu Ala Asp Leu Asp Lys Glu Glu Lys Glu Lys Asp Trp Tyr Tyr Ala
145 150 155 160
Gln Leu Gln Asn Leu Thr Lys Arg Ile Asp Ser Leu Pro Leu Thr Glu
165 170 175
Asn Phe Ser Leu Gln Thr Asp Met Thr Arg Arg Gln Leu Glu Tyr Glu
180 185 190
Ala Arg Gln Ile Arg Val Ala Met Glu Glu Gln Leu Gly Thr Cys Gln
195 200 205
Asp Met Glu Lys Arg Ala Gln Arg Arg Ile Ala Arg Ile Gln Gln Ile
210 215 220
Glu Lys Asp Ile Leu Arg Ile Arg Gln Leu Leu Gln Ser Gln Ala Thr
225 230 235 240

AA 14

SECRET - 6842460

Glu Ala Glu Arg Ser Ser Gln Asn Lys His Glu Thr Gly Ser His Asp
245 250 255

Ala Glu Arg Gln Asn Glu Gly Gln Gly Val Gly Glu Ile Asn Met Ala
260 265 270

Thr Ser Gly Asn Gly Gln Gly Ser Thr Thr Arg Met Asp His Glu Thr
275 280 285

Ala Ser Val Leu Ser Ser Ser Ser Thr His Ser Ala Pro Arg Arg Leu
290 295 300

Thr Ser His Leu Gly Thr Lys Val Glu Met Val Tyr Ser Leu Leu Ser
305 310 315 320

Met Leu Gly Thr His Asp Lys Asp Asp Met Ser Arg Thr Leu Leu Ala
325 330 335

Met Ser Ser Ser Gln Asp Ser Cys Ile Ser Met Arg Gln Ser Gly Cys
340 345 350

Leu Pro Leu Leu Ile Gln Leu Leu His Gly Asn Asp Lys Asp Ser Val
355 360 365

Leu Leu Gly Asn Ser Arg Gly Ser Lys Glu Ala Arg Ala Arg Ala Ser
370 375 380

Ala Ala Leu His Asn Ile Ile His Ser Gln Pro Asp Asp Lys Arg Gly
385 390 395 400

Arg Arg Glu Ile Arg Val Leu His Leu Leu Glu Gln Ile Arg Ala Tyr
405 410 415

Cys Glu Thr Cys Trp Glu Trp Gln Glu Ala His Glu Pro Gly Met Asp
420 425 430

Gln Asp Lys Asn Pro Met Pro Ala Pro Val Glu His Gln Ile Cys Pro
435 440 445

Ala Val Cys Val Leu Met Lys Leu Ser Phe Asp Glu Glu His Arg His
450 455 460

Ala Met Asn Glu Leu Gly Gly Leu Gln Ala Ile Ala Glu Leu Leu Gln
465 470 475 480

Val Asp Cys Glu Met Tyr Gly Leu Thr Asn Asp His Tyr Ser Ile Thr
485 490 495

Leu Arg Arg Tyr Ala Gly Met Ala Leu Thr Asn Leu Thr Phe Gly Asp
500 505 510

Val Ala Asn Lys Ala Thr Leu Cys Ser Met Lys Gly Cys Met Arg Ala
515 520 525

Leu Val Ala Gln Leu Lys Ser Glu Ser Glu Asp Leu Gln Gln Val Ile

AP 14

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530 535 540
Ala Ser Val Leu Arg Asn Leu Ser Trp Arg Ala Asp Val Asn Ser Lys
545 550 555 560
Lys Thr Leu Arg Glu Val Gly Ser Val Lys Ala Leu Met Glu Cys Ala
565 570 575
Leu Glu Val Lys Lys Glu Ser Thr Leu Lys Ser Val Leu Ser Ala Leu
580 585 590
Trp Asn Leu Ser Ala His Cys Thr Glu Asn Lys Ala Asp Ile Cys Ala
595 600 605
Val Asp Gly Ala Leu Ala Phe Leu Val Gly Thr Leu Thr Tyr Arg Ser
610 615 620
Gln Thr Asn Thr Leu Ala Ile Ile Glu Ser Gly Gly Gly Ile Leu Arg
625 630 635 640
Asn Val Ser Ser Leu Ile Ala Thr Asn Glu Asp His Arg Gln Ile Leu
645 650 655
Arg Glu Asn Asn Cys Leu Gln Thr Leu Leu Gln His Leu Lys Ser His
660 665 670
Ser Leu Thr Ile Val Ser Asn Ala Cys Gly Thr Leu Trp Asn Leu Ser
675 680 685
Ala Arg Asn Pro Lys Asp Gln Glu Ala Leu Trp Asp Met Gly Ala Val
690 695 700
Ser Met Leu Lys Asn Leu Ile His Ser Lys His Lys Met Ile Ala Met
705 710 715 720
Gly Ser Ala Ala Ala Leu Arg Asn Leu Met Ala Asn Arg Pro Ala Lys
725 730 735
Tyr Lys Asp Ala Asn Ile Met Ser Pro Gly Ser Ser Leu Pro Ser Leu
740 745 750
His Val Arg Lys Gln Lys Ala Leu Glu Ala Glu Leu Asp Ala Gln His
755 760 765
Leu Ser Glu Thr Phe Asp Asn Ile Asp Asn Leu Ser Pro Lys Ala Ser
770 775 780
His Arg Ser Lys Gln Arg His Lys Gln Ser Leu Tyr Gly Asp Tyr Val
785 790 795 800
Phe Asp Thr Asn Arg His Asp Asp Asn Arg Ser Asp Asn Phe Asn Thr
805 810 815
Gly Asn Met Thr Val Leu Ser Pro Tyr Leu Asn Thr Thr Val Leu Pro

820 825 830
 Ser Ser Ser Ser Ser Arg Gly Ser Leu Asp Ser Ser Arg Ser Glu Lys
 835 840 845
 Asp Arg Ser Leu Glu Arg Glu Arg Gly Ile Gly Leu Gly Asn Tyr His
 850 855 860
 Pro Ala Thr Glu Asn Pro Gly Thr Ser Ser Lys Arg Gly Leu Gln Ile
 865 870 875 880
 Ser Thr Thr Ala Ala Gln Ile Ala Lys Val Met Glu Glu Val Ser Ala
 885 890 895
 Ile His Thr Ser Gln Glu Asp Arg Ser Ser Gly Ser Thr Thr Glu Leu
 900 905 910
 His Cys Val Thr Asp Glu Arg Asn Ala Leu Arg Arg Ser Ser Ala Ala
 915 920 925
 His Thr His Ser Asn Thr Tyr Asn Phe Thr Lys Ser Glu Asn Ser Asn
 930 935 940
 Arg Thr Cys Ser Met Pro Tyr Ala Lys Leu Glu Tyr Lys Arg Ser Ser
 945 950 955 960
 Asn Asp Ser Leu Asn Ser Val Ser Ser Ser Asp Gly Tyr Gly Lys Arg
 965 970 975
 Gly Gln Met Lys Pro Ser Ile Glu Ser Tyr Ser Glu Asp Asp Glu Ser
 980 985 990
 Lys Phe Cys Ser Tyr Gly Gln Tyr Pro Ala Asp Leu Ala His Lys Ile
 995 1000 1005
 His Ser Ala Asn His Met Asp Asp Asn Asp Gly Glu Leu Asp Thr Pro
 1010 1015 1020
 Ile Asn Tyr Ser Leu Lys Tyr Ser Asp Glu Gln Leu Asn Ser Gly Arg
 1025 1030 1035 1040
 Gln Ser Pro Ser Gln Asn Glu Arg Trp Ala Arg Pro Lys His Ile Ile
 1045 1050 1055
 Glu Asp Glu Ile Lys Gln Ser Glu Gln Arg Gln Ser Arg Asn Gln Ser
 1060 1065 1070
 Thr Thr Tyr Pro Val Tyr Thr Glu Ser Thr Asp Asp Lys His Leu Lys
 1075 1080 1085
 Phe Gln Pro His Phe Gly Gln Gln Glu Cys Val Ser Pro Tyr Arg Ser
 1090 1095 1100
 Arg Gly Ala Asn Gly Ser Glu Thr Asn Arg Val Gly Ser Asn His Gly

AA14

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1105 1110 1115 1120
 Ile Asn Gln Asn Val Ser Gln Ser Leu Cys Gln Glu Asp Asp Tyr Glu
 1125 1130 1135
 Asp Asp Lys Pro Thr Asn Tyr Ser Glu Arg Tyr Ser Glu Glu Glu Gln
 1140 1145 1150
 His Glu Glu Glu Glu Arg Pro Thr Asn Tyr Ser Ile Lys Tyr Asn Glu
 1155 1160 1165
 Glu Lys Arg His Val Asp Gln Pro Ile Asp Tyr Ser Leu Lys Tyr Ala
 1170 1175 1180
 Thr Asp Ile Pro Ser Ser Gln Lys Gln Ser Phe Ser Phe Ser Lys Ser
 1185 1190 1195 1200
 Ser Ser Gly Gln Ser Ser Lys Thr Glu His Met Ser Ser Ser Ser Glu
 1205 1210 1215
 Asn Thr Ser Thr Pro Ser Ser Asn Ala Lys Arg Gln Asn Gln Leu His
 1220 1225 1230
 Pro Ser Ser Ala Gln Ser Arg Ser Gly Gln Pro Gln Lys Ala Ala Thr
 1235 1240 1245
 Cys Lys Val Ser Ser Ile Asn Gln Glu Thr Ile Gln Thr Tyr Cys Val
 1250 1255 1260
 Glu Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu Ser Ser Leu
 1265 1270 1275 1280
 Ser Ser Ala Glu Asp Glu Ile Gly Cys Asn Gln Thr Thr Gln Glu Ala
 1285 1290 1295
 Asp Ser Ala Asn Thr Leu Gln Ile Ala Glu Ile Lys Glu Lys Ile Gly
 1300 1305 1310
 Thr Arg Ser Ala Glu Asp Pro Val Ser Glu Val Pro Ala Val Ser Gln
 1315 1320 1325
 His Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser
 1330 1335 1340
 Glu Ser Ala Arg His Lys Ala Val Glu Phe Ser Ser Gly Ala Lys Ser
 1345 1350 1355 1360
 Pro Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr
 1365 1370 1375
 Val Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser
 1380 1385 1390
 Leu Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu

AP 14

66377-6842460

AA 14

66877" 6842460

1395	1400	1405
Pro Cys Ser Gly Met Val	Ser Gly Ile Ile Ser	Pro Ser Asp Leu Pro
1410	1415	1420
Asp Ser Pro Gly Gln Thr	Met Pro Pro Ser Arg Ser Lys Thr Pro	Pro
1425	1430	1435 1440
Pro Pro Pro Gln Thr Ala Gln Thr Lys	Arg Glu Val Pro Lys Asn Lys	
1445	1450	1455
Ala Pro Thr Ala Glu Lys Arg	Glu Ser Gly Pro Lys Gln Ala Ala Val	
1460	1465	1470
Asn Ala Ala Val Gln Arg Val	Gln Val Leu Pro Asp Ala Asp Thr Leu	
1475	1480	1485
Leu His Phe Ala Thr Glu Ser Thr	Pro Asp Gly Phe Ser Cys Ser Ser	
1490	1495	1500
Ser Leu Ser Ala Leu Ser Leu Asp	Glu Pro Phe Ile Gln Lys Asp Val	
1505	1510	1515 1520
Glu Leu Arg Ile Met Pro Pro Val	Gln Glu Asn Asp Asn Gly Asn Glu	
1525	1530	1535
Thr Glu Ser Glu Gln Pro Lys Glu	Ser Asn Glu Asn Gln Glu Lys Glu	
1540	1545	1550
Ala Glu Lys Thr Ile Asp Ser Glu	Lys Asp Leu Leu Asp Asp Ser Asp	
1555	1560	1565
Asp Asp Asp Ile Glu Ile Leu Glu	Glu Cys Ile Ile Ser Ala Met Pro	
1570	1575	1580
Thr Lys Ser Ser Arg Lys Ala Lys Lys	Pro Ala Gln Thr Ala Ser Lys	
1585	1590	1595 1600
Leu Pro Pro Pro Val Ala Arg Lys	Pro Ser Gln Leu Pro Val Tyr Lys	
1605	1610	1615
Leu Leu Pro Ser Gln Asn Arg Leu	Gln Pro Gln Lys His Val Ser Phe	
1620	1625	1630
Thr Pro Gly Asp Asp Met Pro Arg	Val Tyr Cys Val Glu Gly Thr Pro	
1635	1640	1645
Ile Asn Phe Ser Thr Ala Thr Ser	Leu Ser Asp Leu Thr Ile Glu Ser	
1650	1655	1660
Pro Pro Asn Glu Leu Ala Ala Gly	Glu Gly Val Arg Gly Gly Ala Gln	
1665	1670	1675 1680
Ser Gly Glu Phe Glu Lys Arg Asp	Thr Ile Pro Thr Glu Gly Arg Ser	

RA 14

09442469-1139

1685	1690	1695
Thr Asp Glu Ala Gln Gly Gly Lys	Thr Ser Ser Val Thr Ile Pro Glu	
1700	1705	1710
Leu Asp Asp Asn Lys Ala Glu Glu Gly Asp Ile Leu Ala Glu Cys Ile		
1715	1720	1725
Asn Ser Ala Met Pro Lys Gly Lys Ser His Lys Pro Phe Arg Val Lys		
1730	1735	1740
Lys Ile Met Asp Gln Val Gln Gln Ala Ser Ala Ser Ser Ser Ala Pro		
1745	1750	1755
Asn Lys Asn Gln Leu Asp Gly Lys Lys Lys Lys Pro Thr Ser Pro Val		
1765	1770	1775
Lys Pro Ile Pro Gln Asn Thr Glu Tyr Arg Thr Arg Val Arg Lys Asn		
1780	1785	1790
Ala Asp Ser Lys Asn Asn Leu Asn Ala Glu Arg Val Phe Ser Asp Asn		
1795	1800	1805
Lys Asp Ser Lys Lys Gln Asn Leu Lys Asn Asn Ser Lys Asp Phe Asn		
1810	1815	1820
Asp Lys Leu Pro Asn Asn Glu Asp Arg Val Arg Gly Ser Phe Ala Phe		
1825	1830	1835
Asp Ser Pro His His Tyr Thr Pro Ile Glu Gly Thr Pro Tyr Cys Phe		
1845	1850	1855
Ser Arg Asn Asp Ser Leu Ser Ser Leu Asp Phe Asp Asp Asp Val		
1860	1865	1870
Asp Leu Ser Arg Glu Lys Ala Glu Leu Arg Lys Ala Lys Glu Asn Lys		
1875	1880	1885
Glu Ser Glu Ala Lys Val Thr Ser His Thr Glu Leu Thr Ser Asn Gln		
1890	1895	1900
Gln Ser Ala Asn Lys Thr Gln Ala Ile Ala Lys Gln Pro Ile Asn Arg		
1905	1910	1915
Gly Gln Pro Lys Pro Ile Leu Gln Lys Gln Ser Thr Phe Pro Gln Ser		
1925	1930	1935
Ser Lys Asp Ile Pro Asp Arg Gly Ala Ala Thr Asp Glu Lys Leu Gln		
1940	1945	1950
Asn Phe Ala Ile Glu Asn Thr Pro Val Cys Phe Ser His Asn Ser Ser		
1955	1960	1965
Leu Ser Ser Leu Ser Asp Ile Asp Gln Glu Asn Asn Asn Lys Glu Asn		
1970	1975	1980

Glu Pro Ile Lys Glu Thr Glu Pro Pro Asp Ser Gln Gly Glu Pro Ser
 1985 1990 1995 2000
 Lys Pro Gln Ala Ser Gly Tyr Ala Pro Lys Ser Phe His Val Glu Asp
 2005 2010 2015
 Thr Pro Val Cys Phe Ser Arg Asn Ser Ser Leu Ser Ser Leu Ser Ile
 2020 2025 2030
 Asp Ser Glu Asp Asp Leu Leu Gln Glu Cys Ile Ser Ser Ala Met Pro
 2035 2040 2045
 Lys Lys Lys Lys Pro Ser Arg Leu Lys Gly Asp Asn Glu Lys His Ser
 2050 2055 2060
 Pro Arg Asn Met Gly Gly Ile Leu Gly Glu Asp Leu Thr Leu Asp Leu
 2065 2070 2075 2080
 Lys Asp Ile Gln Arg Pro Asp Ser Glu His Gly Leu Ser Pro Asp Ser
 2085 2090 2095
 Glu Asn Phe Asp Trp Lys Ala Ile Gln Glu Gly Ala Asn Ser Ile Val
 2100 2105 2110
 Ser Ser Leu His Gln Ala Ala Ala Ala Cys Leu Ser Arg Gln Ala
 2115 2120 2125
 Ser Ser Asp Ser Asp Ser Ile Leu Ser Leu Lys Ser Gly Ile Ser Leu
 2130 2135 2140
 Gly Ser Pro Phe His Leu Thr Pro Asp Gln Glu Glu Lys Pro Phe Thr
 2145 2150 2155 2160
 Ser Asn Lys Gly Pro Arg Ile Leu Lys Pro Gly Glu Lys Ser Thr Leu
 2165 2170 2175
 Glu Thr Lys Lys Ile Glu Ser Glu Ser Lys Gly Ile Lys Gly Gly Lys
 2180 2185 2190
 Lys Val Tyr Lys Ser Leu Ile Thr Gly Lys Val Arg Ser Asn Ser Glu
 2195 2200 2205
 Ile Ser Gly Gln Met Lys Gln Pro Leu Gln Ala Asn Met Pro Ser Ile
 2210 2215 2220
 Ser Arg Gly Arg Thr Met Ile His Ile Pro Gly Val Arg Asn Ser Ser
 2225 2230 2235 2240
 Ser Ser Thr Ser Pro Val Ser Lys Lys Gly Pro Pro Leu Lys Thr Pro
 2245 2250 2255
 Ala Ser Lys Ser Pro Ser Glu Gly Gln Thr Ala Thr Thr Ser Pro Arg
 2260 2265 2270

Gly Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg
2545 2550 2555 2560

Val Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ser Ile Leu Ser Ala
 2565 2570 2575
 Ser Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val
 2580 2585 2590
 Asn Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala
 2595 2600 2605
 Lys Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn
 2610 2615 2620
 Ser Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser
 2625 2630 2635 2640
 Lys Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp
 2645 2650 2655
 Val Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly
 2660 2665 2670
 Arg Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu
 2675 2680 2685
 Lys Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln
 2690 2695 2700
 Asn Val Gly Asn Gly Ser Val Pro Met Arg Thr Val Gly Leu Glu Asn
 2705 2710 2715 2720
 Arg Leu Asn Ser Phe Ile Gln Val Asp Ala Pro Asp Gln Lys Gly Thr
 2725 2730 2735
 Glu Ile Lys Pro Gly Gln Asn Asn Pro Val Pro Val Ser Glu Thr Asn
 2740 2745 2750
 Glu Ser Ser Ile Val Glu Arg Thr Pro Phe Ser Ser Ser Ser Ser Ser
 2755 2760 2765
 Lys His Ser Ser Pro Ser Gly Thr Val Ala Ala Arg Val Thr Pro Phe
 2770 2775 2780
 Asn Tyr Asn Pro Ser Pro Arg Lys Ser Ser Ala Asp Ser Thr Ser Ala
 2785 2790 2795 2800
 Arg Pro Ser Gln Ile Pro Thr Pro Val Asn Asn Asn Thr Lys Lys Arg
 2805 2810 2815
 Asp Ser Lys Thr Asp Ser Thr Glu Ser Ser Gly Thr Gln Ser Pro Lys
 2820 2825 2830
 Arg His Ser Gly Ser Tyr Leu Val Thr Ser Val
 2835 2840

AA 14

SECRET 684249-1360

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (B) CLONE: ral2(yeast)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Thr Gly Ala Lys Gly Leu Gln Leu Arg Ala Leu Arg Arg Ile Ala
1 5 10 15
Arg Ile Glu Gln Gly Gly Thr Ala Ile Ser Pro Thr Ser Pro Leu
 20 25 30

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: m3(mAChR)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Tyr Trp Arg Ile Tyr Lys Glu Thr Glu Lys Arg Thr Lys Glu Leu
1 5 10 15
Ala Gly Leu Gln Ala Ser Gly Thr Glu Ala Glu Thr Glu
 20 25

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:
(B) CLONE: MCC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Leu Tyr Pro Asn Leu Ala Glu Glu Arg Ser Arg Trp Glu Lys Glu Leu
1 5 10 15
Ala Gly Leu Arg Glu Glu Asn Glu Ser Leu Thr Ala Met
20 25

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTATCAAGAC TGTGACTTTT AATTGTAGTT TATCCATTTT

40

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

09442439-11899

AA 14

TTTAGAATTT CATGTAATA TATTGTGTTT TTTTAAACAG

40

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTAGATTTTA AAAAGGTGTT TTAAATAAT TTTTAAAGCT

40

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AAGCAATTGT TGTATAAAA CTTGTTTCTA TTTTATTAG

40

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTAACCTTTC TTCATATAGT AAACATTGCC TTGTGTACTC

40

AA14

66877 6642460

PP 14
66877 6842460

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

NNNNNNNNNN NNNGTCCCTT TTTTAAAAA AAAAAAATAG

40

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAAGTAACT TGGCAGTACA ACTTATTTGA AACTTTAATA

40

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATACAAGATA TTGATACTTT TTTATTATTT GTGGTTTTAG

40

(2) INFORMATION FOR SEQ ID NO:19:

- AA14
- 66311" 642460
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTAAGTTACT TGTTTCTAAG TGATAAAACA GYGAAGAGCT

40

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AATAAAAACA TAACTAATTA GGTTCCTTGT TTTATTTTAG

40

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTTAGTAAAT TSCCTTTTTT GTTTGTGGGT ATAAAAATAG

40

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACCATTTTGG CATGTACTGA TGTAACTCC ATCTTAACAG

40

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTAAATAAAT TATTTTATCA TATTTTAA AATTATTTAA

40

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CATGATGTTA TCTGTATTTA CCTATAGTCT AAATTATACC ATCTATAATG TGCTTAATTT

60

TTAG

64

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

AA14

66377-6842460

- (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTAACAGAAG ATTACAAACC CTGGTCACTA ATGCCATGAC TACTTTGCTA AG

52

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGATATTAAA GTCGTAATTT TGTTCCTAAA CTCATTTGGC CCACAG

46

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GTATGTTCTC TATAGTGAC ATCGTAGTGC ATGTTTCAAA

40

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs

77414
66877 6842460

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CATCATTGCT CTTCAAATAA CAAAGCATT TGGTTTATGT TGATTTTATT TTTCAG

56

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTAAGACAAA AATGTTTTTT AATGACATAG ACAATTACTG GTG

43

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTAGATGATT GTCTTTTCC TCTTGCCCTT TTAAATTAG

40

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

HA 164

66877 6342460

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTATGTTTTT ATAACATGTA TTTCTTAAGA TAGCTCAGGT ATGA

44

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTTGGCTTC AAGTTGNCTT TTAAATGATC CTCTATTCTG TATTTAATTT ACAG

54

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTACTATTTA GAATTCACCC TGTTTTTCTT TTTTCTCTT TTCTTTGAGG CAGGGTCTCA

60

CTCTG

65

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid

AA14

66377 6642460

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCAACTAGTA TGATTTTATG TATAAATTAA TCTAAAATTG ATTAATTTCC AG

52

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: ~~Homo sapiens~~

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GTACCTTTGA AAACATTTAG TACTATAATA TGAATTTCAT GT

42

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CCAACTCNAA TTAGATGACC CATATTCAGA AACTTACTAG

40

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTATATATAG AGTTTTATAT TACTTTTAAA GTACAGAATT CATACTCTCA AAAA

54

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATTGTGACCT TAATTTGTG ATCTCTTGAT TTTTATTCA G

41

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCCCCGCCTG CCGCTCTC

18

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

7A14

66877" 6842460

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GCAGCGGCGG CTCCCGTG

18

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GTGAACGGCT CTCATGCTGC

20

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACGTGCGGGG AGGAATGGA

19

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

7414

09442459.1.1899

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATGATATCTT ACCAAATGAT ATAC

24

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTATTCCTAC TTCTTCTATA CAG

23

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TACCCATGCT GGCTCTTTT C

21

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

6631121634460

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- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TGGGGCCATC TTGTCCTGA

20

- (2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACATTAGGCA CAAAGCTTGC AA

22

- (2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ATCAAGCTCC AGTAAGAAGG TA

22

- (2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:

66377-6842460

7714

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TGCGGCTCCT GGGTTGTTG

19

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCCCCCTTCCT TTCTGAGGAC

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTTCTCCTG CCTCTTACTG C

21

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

17/14

66377 68424460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGACACCCC CCATTCCTC

20

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCACTTAAAG CACATATATT TAGT

24

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTATGGAAAA TAGTGAAGAA CC

22

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTCTTAAGTC CTGTTTTTCT TTG

24

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TTTAGAACCT TTTTGTGTT GTG

23

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CTCAGATTAT AACTAAGCC TAAC

24

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

2044439-11399
SECRET

CATGTCTCTT ACAGTAGTAC CA

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

AGGTCCAAGG GTAGCCAAGG

20

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TAAAAATGGA TAAACTACAA TTAAAAG

27

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

AAATACAGAA TCATGTCTTG AAGT

24

668111 6342460

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(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ACACCTAAAG ATGACAATTT GAG

23

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TAACTTAGAT AGCAGTAATT TCCC

24

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACAATAAACT GGAGTACACA AGG

23

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ATAGGTCATT GCTTCTTGCT GAT

23

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TGAATTTTAA TGGATTACCT AGGT

24

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTTTTTTTGC TTTTACTGAT TAACG

25

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TGTAATTCAT TTTATTCCTA ATAGCTC

27

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GGTAGCCATA GTATGATTAT TTCT

24

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CTACCTATTT TTATACCCAC AAAC

24

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AAGAAAGCCT ACACCATTTT TGC

23

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GATCATTCTT AGAACCATCT TGC

23

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ACCTATAGTC TAAATTATAC CATC

24

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs

AA14

663116344460

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTCATGGCAT TAGTGACCAG

20

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

AGTCGTAATT TTGTTTCTAA ACTC

24

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TGAAGGACTC GGATTTCACG C

21

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TCATTCACTC ACAGCCTGAT GAC

23

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GCTTTGAAAC ATGCACTACG AT

22

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AAACATCATT GCTCTTCAAA TAAC

24

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

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668777 6842460

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TACCATGATT TAAAAATCCA CCAG

24

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GATGATTGTC TTTTCCTCT TGC

23

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CTGAGCTATC TTAAGAAATA CATG

24

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TTTTAAATGA TCCTCTATTC TGTAT

25

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ACAGAGTCAG ACCCTGCCTC AAAG

24

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TTTCTATTCT TACTGCTAGC ATT

23

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

AA14

66877-6844650

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ATACACAGGT AAGAAATTAG GA

22

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TAGATGACCC ATATTCTGTT TC

22

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CAATTAGGTC TTTTGAGAG TA

22

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

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668777 6642460

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTTACTGCAT ACACATTGTG AC

22

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GCTTTTGTGTT TCCTAACATG AAG

23

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TCTCCCACAG GTAATACTCC C

21

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

8814

66377-684460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GCTAGAACTG AATGGGGTAC G

21

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CAGGACAAAA TAATCCTGTC CC

22

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATTTTCTTAG TTTCATTCTT CCTC

24

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

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66877-6844650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

AGAAGGATCC CTTGTGCAGT GTGGA

25

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GACAGGATCC TGAAGCTGAG TTTG

24

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

TCAGAAAGTG CTGAAGAG

18

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

BB14
66811"6842460

GGAATAATTA GGTCTCCAA

19

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GCAAATCCTA AGAGAGAACA A

21

(2) INFORMATION FOR SEQ ID NO: 100:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GATGGCAAGC TTGAGCCAG

19

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GTTCCAGCAG TGTCACAG

18

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GGGAGATTTC GCTCCTGA

18

GGGAGATTTC GCTCCTGA